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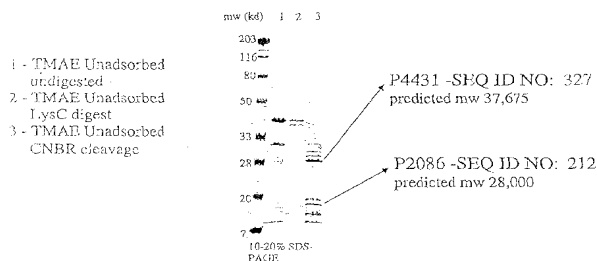
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[Continued on next page]

(54) Title: NOVEL IMMUNOGENIC COMPOSITIONS FOR THE PREVENTION AND TREATMENT OF MENINGOCOCCAL DISEASE

A Identification of Components in the Unadsorbed TMAE Fraction: SDS-PAGE Isolation of Peptides
(CNBR Cleavage of Unadsorbed TMAE Fraction followed by SDS-PAGE and N-term sequencing of fragments from PVDF blot)



B Identification of Components in the Unadsorbed TMAE Fraction: Reverse Phase Isolation of Peptides

Enzymatic digestion of unadsorbed TMAE fraction followed by reverse phase chromatography separation of peptides and direct N-terminal sequencing

Enzymatic Digest	Retention Time of Peptide (min)	Molecular Weight of Peptide (d)	N-term. ID
GluC (V8)	6.716	2069.7	P5163
LysC	13.803	3351.2	P4431
LysC	13.800	3351.2	P2086
ArgC	6.860	2278.9	P5163

P4431 (SEQ ID NO: 327)
predicted mw 36,775

P2086 (SEQ ID NO: 212)
predicted mw 27,100

P5163 (SEQ ID NO: 328)
predicted mw 7,081

(57) Abstract: The present invention relates to *Neisseria* ORF2086 proteins, crossreactive immunogenic proteins which can be isolated from nesserial strains or prepared recombinantly, including immunogenic portions thereof, biological equivalents thereof, antibodies that immunospecifically bind to the foregoing and nucleic acid sequences encoding each of the foregoing, as well as the use of same in immunogenic compositions that are effective against infection by *Neisseria meningitidis* serogroup B.

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NOVEL IMMUNOGENIC COMPOSITIONS FOR THE PREVENTION AND TREATMENT OF MENINGOCOCCAL DISEASE

Field of the Invention

The present invention relates to *Neisseria* ORF2086 proteins (Subfamily A and Subfamily B), which may be isolated from bacterial strains such as those of *Neisseria species*, including strains of *Neisseria meningitidis* (serogroups A, B, C, D, W-135, X, Y, Z and 29E), *Neisseria gonorrhoeae*, and *Neisseria lactamica*, as well as immunogenic portions and/or biological equivalents of said proteins. The present invention also relates to antibodies that immunospecifically bind to said proteins, immunogenic portions and/or biological equivalents. Further, the present invention relates to isolated polynucleotides comprising nucleic acid sequences encoding any of the foregoing proteins, immunogenic portions, biological equivalents and/or antibodies. Additionally, the present invention relates to immunogenic compositions and their use in preventing, treating and/or diagnosing meningococcal infection caused by *N. meningitidis*, and in particular meningococcal disease caused by *N. meningitidis* serogroup B, as well as methods for preparing said compositions. This invention relates to both recombinant forms and forms isolated from a natural source, as well as both lipidated and non-lipidated forms.

Background of the Invention

Meningococcal meningitis is a devastating disease that can kill children and young adults within hours despite the availability of antibiotics. Pizza *et al.*, 2000, *Science* 287:1816-1820. Meningitis is characterized as an inflammation of the meninges resulting in an intense headache, fever, loss of appetite, intolerance to light and sound, rigidity of muscles, especially in the neck, and in severe cases convulsions, vomiting and delirium leading to death. The symptoms of meningococcal meningitis appear suddenly and culminate in meningococcal septicemia with its characteristic hemorrhagic rash. A rapid diagnosis and immediate

treatment with large doses of antibiotics is critical if there is to be any chance of survival. 2000. *Bantam Medical Dictionary, Third Edition* 302.

Meningococcal meningitis is caused by *Neisseria meningitidis* (the meningococcus), a Gram-negative, capsulated bacterium that has been classified into several pathogenic serogroups including A, B, C, D, W-135, X, Y, Z and 29E. Serogroup B strains of *N. meningitidis* are a major cause of meningococcal disease throughout the world. For example, it is reported in the medical literature that serogroup B is responsible for about 50% of bacterial meningitis in infants and children residing in the United States and Europe. No vaccine currently exists to prevent meningococcal disease caused by *N. meningitidis* serogroup B.

Developing an immunogenic composition for the prevention of serogroup B meningococcal disease has been a challenge to researchers since the work of Goldschneider *et al.* over thirty years ago. Goldschneider *et al.*, 1969, *J. Exp. Med* 129(6):1307-26; Goldschneider *et al.*, 1969, *J. Exp. Med* 129(6):1327-48; Gotschlich *et al.*, 1969, *J. Exp. Med.* 129(6):1385-95; and Gotschlich *et al.*, 1969, *J. Exp. Med.* 129(6):1367-84. Unlike serogroup A disease, which virtually disappeared from North America after World War II, Achtman, M., 1995, *Trends in Microbiology* 3(5):186-92, disease caused by serogroup B and C organisms remains endemic throughout much of the economically developed world. The incidence of disease varies from <1/100,000 where endemic disease is rare to 200/100,000 in high risk populations during epidemics.

Vaccines based on polysaccharide conjugates have been developed against *N. meningitidis* serogroups A and C and appear to be effective in preventing disease. Currently, an immunogenic composition made of capsular polysaccharide from serogroups A, C, Y, & W-135 is available. Ambrosch *et al.*, 1983, Immunogenicity and side-effects of a new tetravalent. *Bulletin of the World Health Organization* 61(2):317-23. However, this immunogenic composition elicits a T-cell independent immune response, is not effective in young children, and provides no coverage for serogroup B strains, which cause upwards of 50% of meningococcal disease.

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Others have also attempted to develop immunogenic compositions using capsular polysaccharides. Recently, immunogenic compositions for serogroup C disease prepared by conjugating the serogroup C capsular material to proteins have been licensed for use in Europe. However, the serogroup B capsule may be unsuitable as a vaccine candidate because the capsule polysaccharide is composed of polysialic acid which bears a similarity to carbohydrate moieties on developing human neural tissues. This sugar moiety is recognized as a self-antigen and is thus poorly immunogenic in humans.

Outer membrane proteins (OMP's) have been developed as alternative vaccine antigens for serogroup B disease. Monoclonal antibody binding to the two variable regions of PorA define the serosubtyping scheme for meningococci. PorA proteins thus serve as the serosubtyping antigens (Abdillahi *et al.*, 1988, *Microbial Pathogenesis* 4(1):27-32) for meningococcal strains and are being actively investigated as components of a serogroup B immunogenic composition (Poolman, 1996, *Adv. Exp. Med. Biol.* 397:73-7), since they can elicit bactericidal antibodies (Saukkonen, 1987, *Microbial Pathogenesis* 3(4):261-7). Bactericidal antibodies are thought to be an indicator of protection and any new immunogenic composition candidate should elicit these functional antibodies.

Studies in humans as well as animals indicate that the serosubtyping antigen, PorA, elicits bactericidal antibodies. However, the immune response to Por A is generally serosubtype specific. In particular, serosubtyping data indicate that an immunogenic composition made of PorAs may require a PorA for each serosubtype to be covered by such an immunogenic composition, perhaps as many as six to nine. Therefore, 6-9 PorAs will be needed to cover 70-80% of serogroup B strains. Thus, the variable nature of this protein requires a multivalent vaccine composition to protect against a sufficient number of meningococcal serosubtype clinical isolates.

Developing an immunogenic composition for serogroup B meningococci has been so difficult that recently several groups have sequenced the genomes from strains representing both serogroups A and B to assist in identifying new immunogenic composition candidates. Tettelin, 2000, *Science*, 287(5459):1809-15;

Pizza *et al.*, 2000, *Science* 287:1816-1820. Identifying new immunogenic composition candidates, even with the knowledge of the neisserial genome, is a challenging process for which adequate mathematical algorithms do not currently exist. In fact, a recent report indicates that despite identifying hundreds of open
5 reading frames (“ORFs”) containing theoretical membrane spanning domains, problems with expression, purification, and inducing surface reactive, and functionally active antibodies have led investigators to only seven candidates for a serogroup B meningococcal immunogenic composition. *See Id.* One of these was previously known.

10 Accordingly, there remains a need for immunogenic compositions that (1) elicit bactericidal antibodies to multiple neisserial strains; (2) react with the surface of multiple strains; (3) confer passive protection against a live challenge; and/or (4) prevent colonization.

Summary of the Invention

15 To meet these and other needs, and in view of its purposes, the present invention provides *Neisseria* ORF2086 proteins (“2086 proteins”), including 2086 Subfamily A proteins and 2086 Subfamily B proteins. Each of the 2086 proteins are proteins that can be isolated from native neisserial strains, including strains of
20 *Neisseria meningitidis* (serogroups A, B, C, D, W-135, X, Y, Z and 29E), *Neisseria gonorrhoeae*, and *Neisseria lactamica*. The 2086 proteins may also be prepared using recombinant technology.

 In particular, the present invention provides the 2086 proteins, immunogenic portions thereof, and/or biological equivalents thereof, antibodies that immunospecifically bind to any of the foregoing, and polynucleotides comprising
25 nucleic acid sequences that encode any of the foregoing. The present invention includes compositions, immunogenic compositions and their use in preventing, treating and/or diagnosing meningococcal infection, and in particular meningococcal disease caused by *N. meningitidis*, as well as methods for preparing said

compositions. The 2086 proteins herein include recombinant forms and forms isolated from a natural source, as well as both lipidated and non-lipidated forms.

The present invention unexpectedly and advantageously provides compositions that (1) elicit bactericidal antibodies to multiple neisserial strains, such as strains of *N. meningitidis*, *N. gonorrhoeae*, and/or *N. lactamica*; (2) react with the surface of multiple strains; (3) confer passive protection against a live challenge; and/or (4) prevent colonization, as well as methods of using said compositions and methods of preparing said compositions. Various embodiments of the invention are described below.

Brief Description of the Drawings

FIG. 1A depicts an SDS-PAGE gel that depicts the two major proteins of the protein fractions obtained from the experiments for identifying neisserial membrane protein extract that is capable of eliciting bactericidal antibodies against heterologous strains.

FIG. 1B depicts the results from the experiments from the identification of the two major proteins by analysis of TMAE Flow Through components by protease digestion and reverse Phase N-terminal sequencing.

FIG. 2 depicts the purification scheme and homogeneity as determined by SDS-PAGE of rLP2086.

FIG. 3 depicts the results from the experiments from the identification of the two major proteins and one minor protein by analysis of TMAE Flow Through components by LC-MS/MS and the corresponding SDS-PAGE.

FIG. 4 is an SDS-PAGE gel from the recombinant expression of 2086 protein.

FIG. 5 is a schematic diagram of plasmid pPX7340, as described in the examples herein.

FIG. 6 is a schematic diagram of plasmid pPX7328 as described in the examples herein.

5 FIG. 7 is a schematic diagram of plasmid pPX7343 as described in the examples herein.

FIG. 8 illustrates N-terminal regions of 2086 gene from various strains.

FIG. 9A is a flow chart showing the preliminary steps in the identification of an immunogenic component in a nesserial strain.

10 FIG. 9B is a flow chart showing the final steps in the identification of an immunogenic component in a nesserial strain.

FIG. 10A is a schematic diagram of the pBAD arabinose inducible promoter which drives the expression of the P4 signal/ORF2086 fusion protein to express a lipidated form of rP2086 as described in the examples herein.

15 FIG. 10B is a schematic diagram of the pET9a-T7 vector for recombinant expression of nonlipidated form of ORF2086.

FIG. 11A is a photograph representing whole cell lysates of *E. coli* B expressing the rLP2086 protein.

20 FIG. 11B is a photograph representing whole cell lysates of *E. coli* B expressing the rP2086 protein.

FIG. 12 is a phylogenetic tree showing the organization of the subfamilies and groups of ORF2086 proteins.

FIG. 13 is a graphical illustration of whole cell ELISA data for the rLP2086 Subfamily A antisera.

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FIG. 14 is a graphical illustration of whole cell ELISA data for the rLP2086 Subfamily B antisera.

FIG. 15 is a graphical illustration of the results of the rLP2086 mixing study - WCE Titers.

5 FIG. 16 is a graphical illustration of the results of the rLP2086/rPorA mixing study - WCE Titers.

FIG. 17 is a Western Blot showing reactivity of rLP2086 mouse antisera to P2086 Subfamily B *N. meningitidis* whole cell lysates.

10 FIG. 18 is a Western Blot showing reactivity of rLP2086 mouse antisera to P2086 Subfamily A *N. meningitidis* and *N. lactamica* whole cell lysates.

Sequence Summary

SEQ ID NOS. For Studied Sequences:

15 SEQ ID NO:1 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from L3 6275 strain when combined with a native leader sequence.

SEQ ID NO:2 amino acid sequence for mature 2086 protein from L3 6275 strain prepared using a native leader sequence.

SEQ ID NO:3 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from L3 6275 when combined with a P4 leader sequence.

20 SEQ ID NO:4 amino acid sequence for mature 2086 protein from L3 6275 strain prepared using a P4 leader sequence.

SEQ ID NO:5 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from L3 6275 strain.

SEQ ID NO:6 amino acid sequence for mature 2086 protein from L3 6275 strain.

SEQ ID NO:7 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from CDC2369 strain when combined with a native leader sequence.

SEQ ID NO:8 amino acid sequence for mature 2086 protein from CDC2369 strain prepared using a native leader sequence.

- 5 SEQ ID NO:9 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from CDC2369 when combined with a P4 leader sequence.

SEQ ID NO:10 amino acid sequence for mature 2086 protein from CDC2369 strain prepared using a P4 leader sequence.

- 10 SEQ ID NO:11 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from CDC2369 strain.

SEQ ID NO:12 amino acid sequence for mature 2086 protein from CDC2369 strain.

SEQ ID NO:13 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from CDC1034 strain when combined with a native leader sequence.

- 15 SEQ ID NO:14 amino acid sequence for mature 2086 protein from CDC1034 strain prepared using a native leader sequence.

SEQ ID NO:15 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from CDC1034 when combined with a P4 leader sequence.

SEQ ID NO:16 amino acid sequence for mature 2086 protein from CDC1034 strain prepared using a P4 leader sequence.

- 20 SEQ ID NO:17 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from CDC1034 strain.

SEQ ID NO:18 amino acid sequence for mature 2086 protein from CDC1034 strain.

SEQ ID NO:19 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from L4 891 strain when combined with a native leader sequence.

SEQ ID NO:20 amino acid sequence for mature 2086 protein from L4 891 strain prepared using a native leader sequence.

SEQ ID NO:21 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from L4 891 when combined with a P4 leader sequence.

- 5 SEQ ID NO:22 amino acid sequence for mature 2086 protein from L4 891 strain prepared using a P4 leader sequence.

SEQ ID NO:23 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from L4 891 strain.

SEQ ID NO:24 amino acid sequence for mature 2086 protein from L4 891 strain.

- 10 SEQ ID NO:25 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from B16B6 strain when combined with a native leader sequence.

SEQ ID NO:26 amino acid sequence for mature 2086 protein from B16B6 strain prepared using a native leader sequence.

- 15 SEQ ID NO:27 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from B16B6 when combined with a P4 leader sequence.

SEQ ID NO:28 amino acid sequence for mature 2086 protein from B16B6 strain prepared using a P4 leader sequence.

SEQ ID NO:29 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from B16B6 strain.

- 20 SEQ ID NO:30 amino acid sequence for mature 2086 protein from B16B6 strain.

SEQ ID NO:31 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from W135 (ATCC35559) strain when combined with a native leader sequence.

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SEQ ID NO:32 amino acid sequence for mature 2086 protein from W135 (ATCC35559) strain prepared using a native leader sequence.

SEQ ID NO:33 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from W135 (ATCC35559) when combined with a P4 leader sequence.

- 5 SEQ ID NO:34 amino acid sequence for mature 2086 protein from W135 (ATCC35559) strain prepared using a P4 leader sequence.

SEQ ID NO:35 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from W135 (ATCC35559) strain.

- 10 SEQ ID NO:36 amino acid sequence for mature 2086 protein from W135 (ATCC35559) strain.

SEQ ID NO:37 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from C11 strain when combined with a native leader sequence.

SEQ ID NO:38 amino acid sequence for mature 2086 protein from C11 strain prepared using a native leader sequence.

- 15 SEQ ID NO:39 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from C11 when combined with a P4 leader sequence.

SEQ ID NO:40 amino acid sequence for mature 2086 protein from C11 strain prepared using a P4 leader sequence.

- 20 SEQ ID NO:41 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from C11 strain.

SEQ ID NO:42 amino acid sequence for mature 2086 protein from C11 strain.

SEQ ID NO:43 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from Y (ATCC35561) strain when combined with a native leader sequence.

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SEQ ID NO:44 amino acid sequence for mature 2086 protein from Y (ATCC35561) strain prepared using a native leader sequence.

SEQ ID NO:45 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from Y (ATCC35561) when combined with a P4 leader sequence.

- 5 SEQ ID NO:46 amino acid sequence for mature 2086 protein from Y (ATCC35561) strain prepared using a P4 leader sequence.

SEQ ID NO:47 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from Y (ATCC35561) strain.

- 10 SEQ ID NO:48 amino acid sequence for mature 2086 protein from Y (ATCC35561) strain.

SEQ ID NO:49 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M98 250732 strain when combined with a native leader sequence.

SEQ ID NO:50 amino acid sequence for mature 2086 protein from M98 250732 strain prepared using a native leader sequence.

- 15 SEQ ID NO:51 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from M98 250732 when combined with a P4 leader sequence.

SEQ ID NO:52 amino acid sequence for mature 2086 protein from M98 250732 strain prepared using a P4 leader sequence.

- 20 SEQ ID NO:53 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M98 250732 strain.

SEQ ID NO:54 amino acid sequence for mature 2086 protein from M98 250732 strain.

SEQ ID NO:55 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M98 250771 strain when combined with a native leader sequence.

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SEQ ID NO:56 amino acid sequence for mature 2086 protein from M98 250771 strain prepared using a native leader sequence.

SEQ ID NO:57 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from M98 250771 when combined with a P4 leader sequence.

- 5 SEQ ID NO:58 amino acid sequence for mature 2086 protein from M98 250771 strain prepared using a P4 leader sequence.

SEQ ID NO:59 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M98 250771 strain.

- 10 SEQ ID NO:60 amino acid sequence for mature 2086 protein from M98 250771 strain.

SEQ ID NO:61 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from CDC1135 strain when combined with a native leader sequence.

SEQ ID NO:62 amino acid sequence for mature 2086 protein from CDC1135 strain prepared using a native leader sequence.

- 15 SEQ ID NO:63 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from CDC1135 when combined with a P4 leader sequence.

SEQ ID NO:64 amino acid sequence for mature 2086 protein from CDC1135 strain prepared using a P4 leader sequence.

- 20 SEQ ID NO:65 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from CDC1135 strain.

SEQ ID NO:66 amino acid sequence for mature 2086 protein from CDC1135 strain.

SEQ ID NO:67 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M97 252153 strain when combined with a native leader sequence.

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SEQ ID NO:68 amino acid sequence for mature 2086 protein from M97 252153 strain prepared using a native leader sequence.

SEQ ID NO:69 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from M97 252153 when combined with a P4 leader sequence.

- 5 SEQ ID NO:70 amino acid sequence for mature 2086 protein from M97 252153 strain prepared using a P4 leader sequence.

SEQ ID NO:71 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M97 252153 strain.

- 10 SEQ ID NO:72 amino acid sequence for mature 2086 protein from M97 252153 strain.

SEQ ID NO:73 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from CDC1610 strain when combined with a native leader sequence.

SEQ ID NO:74 amino acid sequence for mature 2086 protein from CDC1610 strain prepared using a native leader sequence.

- 15 SEQ ID NO:75 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from CDC1610 when combined with a P4 leader sequence.

SEQ ID NO:76 amino acid sequence for mature 2086 protein from CDC1610 strain prepared using a P4 leader sequence.

- 20 SEQ ID NO:77 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from CDC1610 strain.

SEQ ID NO:78 amino acid sequence for mature 2086 protein from CDC1610 strain.

SEQ ID NO:79 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from CDC1492 strain when combined with a native leader sequence.

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SEQ ID NO:80 amino acid sequence for mature 2086 protein from CDC1492 strain prepared using a native leader sequence.

SEQ ID NO:81 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from CDC1492 when combined with a P4 leader sequence.

- 5 SEQ ID NO:82 amino acid sequence for mature 2086 protein from CDC1492 strain prepared using a P4 leader sequence.

SEQ ID NO:83 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from CDC1492 strain.

SEQ ID NO:84 amino acid sequence for mature 2086 protein from CDC1492 strain.

- 10 SEQ ID NO:85 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from L8 M978 strain when combined with a native leader sequence.

SEQ ID NO:86 amino acid sequence for mature 2086 protein from L8 M978 strain prepared using a native leader sequence.

- 15 SEQ ID NO:87 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from L8 M978 when combined with a P4 leader sequence.

SEQ ID NO:88 amino acid sequence for mature 2086 protein from L8 M978 strain prepared using a P4 leader sequence.

SEQ ID NO:89 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from L8 M978 strain.

- 20 SEQ ID NO:90 amino acid sequence for mature 2086 protein from L8 M978 strain.

SEQ ID NO:91 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M97 252988 strain when combined with a native leader sequence.

SEQ ID NO:92 amino acid sequence for mature 2086 protein from M97 252988 strain prepared using a native leader sequence.

-15-

SEQ ID NO:93 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from M97 252988 when combined with a P4 leader sequence.

SEQ ID NO:94 amino acid sequence for mature 2086 protein from M97 252988 strain prepared using a P4 leader sequence.

- 5 SEQ ID NO:95 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M97 252988 strain.

SEQ ID NO:96 amino acid sequence for mature 2086 protein from M97 252988 strain.

- 10 SEQ ID NO:97 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M97 252697 strain when combined with a native leader sequence.

SEQ ID NO:98 amino acid sequence for mature 2086 protein from M97 252697 strain prepared using a native leader sequence.

SEQ ID NO:99 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from M97 252697 when combined with a P4 leader sequence.

- 15 SEQ ID NO:100 amino acid sequence for mature 2086 protein from M97 252697 strain prepared using a P4 leader sequence.

SEQ ID NO:101 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M97 252697 strain.

- 20 SEQ ID NO:102 amino acid sequence for mature 2086 protein from M97 252697 strain.

SEQ ID NO:103 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from 6557 strain when combined with a native leader sequence.

SEQ ID NO:104 amino acid sequence for mature 2086 protein from 6557 strain prepared using a native leader sequence.

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SEQ ID NO:105 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from 6557 when combined with a P4 leader sequence.

SEQ ID NO:106 amino acid sequence for mature 2086 protein from 6557 strain prepared using a P4 leader sequence.

- 5 SEQ ID NO:107 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from 6557 strain.

SEQ ID NO:108 amino acid sequence for mature 2086 protein from 6557 strain.

SEQ ID NO:109 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from 2996 strain when combined with a native leader sequence.

- 10 SEQ ID NO:110 amino acid sequence for mature 2086 protein from 2996 strain prepared using a native leader sequence.

SEQ ID NO:111 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from 2996 when combined with a P4 leader sequence.

- 15 SEQ ID NO:112 amino acid sequence for mature 2086 protein from 2996 strain prepared using a P4 leader sequence.

SEQ ID NO:113 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from 2996 strain.

SEQ ID NO:114 amino acid sequence for mature 2086 protein from 2996 strain.

- 20 SEQ ID NO:115 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M97 252976 strain when combined with a native leader sequence.

SEQ ID NO:116 amino acid sequence for mature 2086 protein from M97 252976 strain prepared using a native leader sequence.

SEQ ID NO:117 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from M97 252976 when combined with a P4 leader sequence.

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SEQ ID NO:118 amino acid sequence for mature 2086 protein from M97 252976 strain prepared using a P4 leader sequence.

SEQ ID NO:119 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M97 252976 strain.

- 5 SEQ ID NO:120 amino acid sequence for mature 2086 protein from M97 252976 strain.

SEQ ID NO:121 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M97 251854 strain when combined with a native leader sequence.

- 10 SEQ ID NO:122 amino acid sequence for mature 2086 protein from M97 251854 strain prepared using a native leader sequence.

SEQ ID NO:123 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from M97 251854 when combined with a P4 leader sequence.

SEQ ID NO:124 amino acid sequence for mature 2086 protein from M97 251854 strain prepared using a P4 leader sequence.

- 15 SEQ ID NO:125 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M97 251854 strain.

SEQ ID NO:126 amino acid sequence for mature 2086 protein from M97 251854 strain.

- 20 SEQ ID NO:127 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from CDC1521 strain when combined with a native leader sequence.

SEQ ID NO:128 amino acid sequence for mature 2086 protein from CDC1521 strain prepared using a native leader sequence.

SEQ ID NO:129 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from CDC1521 when combined with a P4 leader sequence.

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SEQ ID NO:130 amino acid sequence for mature 2086 protein from CDC1521 strain prepared using a P4 leader sequence.

SEQ ID NO:131 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from CDC1521 strain.

- 5 SEQ ID NO:132 amino acid sequence for mature 2086 protein from CDC1521 strain.

SEQ ID NO:133 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M98 250622 strain when combined with a native leader sequence.

SEQ ID NO:134 amino acid sequence for mature 2086 protein from M98 250622 strain prepared using a native leader sequence.

- 10 SEQ ID NO:135 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from M98 250622 when combined with a P4 leader sequence.

SEQ ID NO:136 amino acid sequence for mature 2086 protein from M98 250622 strain prepared using a P4 leader sequence.

- 15 SEQ ID NO:137 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M98 250622 strain.

SEQ ID NO:138 amino acid sequence for mature 2086 protein from M98 250622 strain.

SEQ ID NO:139 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from 870446 strain when combined with a native leader sequence.

- 20 SEQ ID NO:140 amino acid sequence for mature 2086 protein from 870446 strain prepared using a native leader sequence.

SEQ ID NO:141 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from 870446 when combined with a P4 leader sequence.

SEQ ID NO:142 amino acid sequence for mature 2086 protein from 870446 strain prepared using a P4 leader sequence.

SEQ ID NO:143 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from 870446 strain.

- 5 SEQ ID NO:144 amino acid sequence for mature 2086 protein from 870446 strain.

SEQ ID NO:145 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M97 253248 strain when combined with a native leader sequence.

SEQ ID NO:146 amino acid sequence for mature 2086 protein from M97 253248 strain prepared using a native leader sequence.

- 10 SEQ ID NO:147 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from M97 253248 when combined with a P4 leader sequence.

SEQ ID NO:148 amino acid sequence for mature 2086 protein from M97 253248 strain prepared using a P4 leader sequence.

- 15 SEQ ID NO:149 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M97 253248 strain.

SEQ ID NO:150 amino acid sequence for mature 2086 protein from M97 253248 strain.

SEQ ID NO:151 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M98 250809 strain when combined with a native leader sequence.

- 20 SEQ ID NO:152 amino acid sequence for mature 2086 protein from M98 250809 strain prepared using a native leader sequence.

SEQ ID NO:153 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from M98 250809 when combined with a P4 leader sequence.

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SEQ ID NO:154 amino acid sequence for mature 2086 protein from M98 250809 strain prepared using a P4 leader sequence.

SEQ ID NO:155 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M98 250809 strain.

- 5 SEQ ID NO:156 amino acid sequence for mature 2086 protein from M98 250809 strain.

SEQ ID NO:157 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from L5 M981 strain when combined with a native leader sequence.

- 10 SEQ ID NO:158 amino acid sequence for mature 2086 protein from L5 M981 strain prepared using a native leader sequence.

SEQ ID NO:159 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from L5 M981 when combined with a P4 leader sequence.

SEQ ID NO:160 amino acid sequence for mature 2086 protein from L5 M981 strain prepared using a P4 leader sequence.

- 15 SEQ ID NO:161 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from L5 M981 strain.

SEQ ID NO:162 amino acid sequence for mature 2086 protein from L5 M981 strain.

SEQ ID NO:163 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from NMB strain when combined with a native leader sequence.

- 20 SEQ ID NO:164 amino acid sequence for mature 2086 protein from NMB strain prepared using a native leader sequence.

SEQ ID NO:165 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from NMB when combined with a P4 leader sequence.

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SEQ ID NO:166 amino acid sequence for mature 2086 protein from NMB strain prepared using a P4 leader sequence.

SEQ ID NO:167 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from NMB strain.

- 5 SEQ ID NO:168 amino acid sequence for mature 2086 protein from NMB strain.

SEQ ID NO:169 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M98 250572 strain when combined with a native leader sequence.

SEQ ID NO:170 amino acid sequence for mature 2086 protein from M98 250572 strain prepared using a native leader sequence.

- 10 SEQ ID NO:171 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from M98 250572 when combined with a P4 leader sequence.

SEQ ID NO:172 amino acid sequence for mature 2086 protein from M98 250572 strain prepared using a P4 leader sequence.

- 15 SEQ ID NO:173 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M98 250572 strain.

SEQ ID NO:174 amino acid sequence for mature 2086 protein from M98 250572 strain.

- 20 SEQ ID NO:175 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from A4 Sanford; M97 251836 PART; M97 251957; M97 251985; M97 252060; M97 251870; M97 251994; M98 250024; M97 251905; M97 251876; M97 251898; or M97 251830 strain when combined with a native leader sequence.

- 25 SEQ ID NO:176 amino acid sequence for mature 2086 protein from A4 Sanford; M97 251836 PART; M97 251957; M97 251985; M97 252060; M97 251870; M97 251994; M98 250024; M97 251905; M97 251876; M97 251898; or M97 251830 strain prepared using a native leader sequence.

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SEQ ID NO:177 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from A4 Sanford; M97 251836 PART; M97 251957; M97 251985; M97 252060; M97 251870; M97 251994; M98 250024; M97 251905; M97 251876; M97 251898; or M97 251830 when combined with a P4 leader sequence.

- 5 SEQ ID NO:178 amino acid sequence for mature 2086 protein from A4 Sanford; M97 251836 PART; M97 251957; M97 251985; M97 252060; M97 251870; M97 251994; M98 250024; M97 251905; M97 251876; M97 251898; or M97 251830 strain prepared using a P4 leader sequence.

- 10 SEQ ID NO:179 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from A4 Sanford; M97 251836 part; M97 251957; M97 251985; M97 252060; M97 251870; M97 251994; M98 250024; M97 251905; M97 251876; M97 251898; or M97 251830 strain.

- 15 SEQ ID NO:180 amino acid sequence for mature 2086 protein from A4 Sanford; M97 251836 PART; M97 251957; M97 251985; M97 252060; M97 251870; M97 251994; M98 250024; M97 251905; M97 251876; M97 251898; or M97 251830 strain.

SEQ ID NO:181 nucleic acid sequence encoding partial amino acid sequence for mature 2086 protein from CDC937 strain when combined with a native leader sequence.

- 20 SEQ ID NO:182 amino acid sequence for mature 2086 protein from CDC937 strain prepared using a native leader sequence.

SEQ ID NO:183 nucleic acid sequence for encoding partial amino acid sequence for mature 2086 protein from CDC937 when combined with a P4 leader sequence.

- 25 SEQ ID NO:184 amino acid sequence for mature 2086 protein from CDC937 strain prepared using a P4 leader sequence.

SEQ ID NO:185 nucleic acid sequence encoding partial amino acid sequence for mature 2086 protein from CDC937 strain.

SEQ ID NO:186 amino acid sequence for mature 2086 protein from CDC937 strain.

SEQ ID NO:187 nucleic acid sequence encoding partial amino acid sequence for mature 2086 protein from M97 252097 strain when combined with a native leader sequence.

- 5 SEQ ID NO:188 amino acid sequence for mature 2086 protein from M97 252097 strain prepared using a native leader sequence.

SEQ ID NO:189 nucleic acid sequence for encoding partial amino acid sequence for mature 2086 protein from M97 252097 when combined with a P4 leader sequence.

- 10 SEQ ID NO:190 amino acid sequence for mature 2086 protein from M97 252097 strain prepared using a P4 leader sequence.

SEQ ID NO:191 nucleic acid sequence encoding partial amino acid sequence for mature 2086 protein from M97 252097 strain.

SEQ ID NO:192 amino acid sequence for mature 2086 protein from M97 252097 strain.

- 15 SEQ ID NO:193 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from 870227 strain when combined with a native leader sequence.

SEQ ID NO:194 amino acid sequence for mature 2086 protein from 870227 strain prepared using a native leader sequence.

- 20 SEQ ID NO:195 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from 870227 when combined with a P4 leader sequence.

SEQ ID NO:196 amino acid sequence for mature 2086 protein from 870227 strain prepared using a P4 leader sequence.

SEQ ID NO:197 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from 870227 strain.

SEQ ID NO:198 amino acid sequence for mature 2086 protein from 870227 strain.

SEQ ID NO:199 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from H355 strain when combined with a native leader sequence.

5 SEQ ID NO:200 amino acid sequence for mature 2086 protein from H355 strain prepared using a native leader sequence.

SEQ ID NO:201 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from H355 when combined with a P4 leader sequence.

SEQ ID NO:202 amino acid sequence for mature 2086 protein from H355 strain prepared using a P4 leader sequence.

10 SEQ ID NO:203 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from H355 strain.

SEQ ID NO:204 amino acid sequence for mature 2086 protein from H355 strain.

SEQ ID NO:205 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from H44_76 strain when combined with a native leader sequence.

15 SEQ ID NO:206 amino acid sequence for mature 2086 protein from H44_76 strain prepared using a native leader sequence.

SEQ ID NO:207 amino acid sequence for mature 2086 protein from H44_76 strain prepared using a P4 leader sequence.

20 SEQ ID NO:208 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from H44_76 strain.

SEQ ID NO:209 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from H44_76 when combined with a P4 leader sequence.

SEQ ID NO:210 amino acid sequence for mature 2086 protein from H44_76 strain.

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SEQ ID NO:211 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from 8529 strain when combined with a native leader sequence.

SEQ ID NO:212 amino acid sequence for mature 2086 protein from 8529 strain prepared using a native leader sequence.

- 5 SEQ ID NO:213 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from 8529 when combined with a P4 leader sequence.

SEQ ID NO:214 amino acid sequence for mature 2086 protein from 8529 strain prepared using a P4 leader sequence.

- 10 SEQ ID NO:215 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from 8529 strain.

SEQ ID NO:216 amino acid sequence for mature 2086 protein from 8529 strain.

SEQ ID NO:217 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from 6940 strain when combined with a native leader sequence.

- 15 SEQ ID NO:218 amino acid sequence for mature 2086 protein from 6940 strain prepared using a native leader sequence.

SEQ ID NO:219 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from 6940 when combined with a P4 leader sequence.

SEQ ID NO:220 amino acid sequence for mature 2086 protein from 6940 strain prepared using a P4 leader sequence.

- 20 SEQ ID NO:221 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from 6940 strain.

SEQ ID NO:222 amino acid sequence for mature 2086 protein from 6940 strain.

SEQ ID NO:223 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M982 strain when combined with a native leader sequence.

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SEQ ID NO:224 amino acid sequence for mature 2086 protein from M982 strain prepared using a native leader sequence.

SEQ ID NO:225 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from M982 when combined with a P4 leader sequence.

- 5 SEQ ID NO:226 amino acid sequence for mature 2086 protein from M982 strain prepared using a P4 leader sequence.

SEQ ID NO:227 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M982 strain.

SEQ ID NO:228 amino acid sequence for mature 2086 protein from M982 strain.

- 10 SEQ ID NO:229 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from 880049 strain when combined with a native leader sequence.

SEQ ID NO:230 amino acid sequence for mature 2086 protein from 880049 strain prepared using a native leader sequence.

- 15 SEQ ID NO:231 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from 880049 when combined with a P4 leader sequence.

SEQ ID NO:232 amino acid sequence for mature 2086 protein from 880049 strain prepared using a P4 leader sequence.

SEQ ID NO:233 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from 880049 strain.

- 20 SEQ ID NO:234 amino acid sequence for mature 2086 protein from 880049 strain.

SEQ ID NO:235 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M97 253524, M97 251885, and M97 251926 strains when combined with a native leader sequence.

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SEQ ID NO:236 amino acid sequence for mature 2086 protein from M97 253524, M97 251885, and M97 251926 strains prepared using a native leader sequence.

5 SEQ ID NO:237 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from M97 253524, M97 251885, and M97 251926 strains when combined with a P4 leader sequence.

SEQ ID NO:238 amino acid sequence for mature 2086 protein from M97 253524, M97 251885, and M97 251926 strains prepared using a P4 leader sequence.

SEQ ID NO:239 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M97 253524, M97 251885, and M97 251926 strains.

10 SEQ ID NO:240 amino acid sequence for mature 2086 protein from M97 253524, M97 251885, and M97 251926 strains.

SEQ ID NO:241 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M98 250670 strain when combined with a native leader sequence.

15 SEQ ID NO:242 amino acid sequence for mature 2086 protein from M98 250670 strain prepared using a native leader sequence.

SEQ ID NO:243 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from M98 250670 when combined with a P4 leader sequence.

SEQ ID NO:244 amino acid sequence for mature 2086 protein from M98 250670 strain prepared using a P4 leader sequence.

20 SEQ ID NO:245 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from M98 250670 strain.

SEQ ID NO:246 amino acid sequence for mature 2086 protein from M98 250670 strain.

25 SEQ ID NO:247 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from CDC1573 strain when combined with a native leader sequence.

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SEQ ID NO:248 amino acid sequence for mature 2086 protein from CDC1573 strain prepared using a native leader sequence.

SEQ ID NO:249 nucleic acid sequence for encoding amino acid sequence for mature 2086 protein from CDC1573 when combined with a P4 leader sequence.

- 5 SEQ ID NO:250 amino acid sequence for mature 2086 protein from CDC1573 strain prepared using a P4 leader sequence.

SEQ ID NO:251 nucleic acid sequence encoding amino acid sequence for mature 2086 protein from CDC1573 strain.

SEQ ID NO:252 amino acid sequence for mature 2086 protein from CDC1573 strain.

- 10 SEQ ID NO:253 partial nucleic acid sequence encoding amino acid sequence for 2086 protein from a strain of *Neisseria lactamica*.

SEQ ID NOS:254 to 259 amino acid sequences associated with proteins of 2086 family of proteins.

SEQ ID NOS:260 to 278 amino acid sequences associated with proteins of 2086

- 15 Subfamily A.

SEQ ID NOS:279 to 299 amino acid sequences associated with proteins of 2086 Subfamily B.

SEQ ID NO:300 is the amino acid consensus sequence corresponding to the 2086 protein family ("2086 proteins") according to an embodiment of the present invention.

- 20 SEQ ID NO:301 is the amino acid consensus sequence corresponding to the 2086 protein Subfamily A according to an embodiment of the present invention.

SEQ ID NO:302 is the amino acid consensus sequence corresponding to the 2086 protein Subfamily B according to an embodiment of the present invention.

SEQ ID NO:303 nucleic acid sequence for a reverse primer with BamHI restriction site (Compound No. 4623).

SEQ ID NO:304 nucleic acid sequence for a forward primer with NdeI restriction site (Compound No. 4624).

5 SEQ ID NO:305 nucleic acid sequence for a forward primer (Compound No. 4625).

SEQ ID NO:306 nucleic acid sequence for a forward primer (Compound No. 5005).

SEQ ID NO:307 nucleic acid sequence for a reverse primer (Compound No. 5007).

SEQ ID NO:308 nucleic acid sequence for a reverse primer with BglII restriction site (Compound No. 5135).

10 SEQ ID NO:309 nucleic acid sequence for a forward primer with BamHI restriction site (Compound No. 5658).

SEQ ID NO:310 nucleic acid sequence for a reverse primer with SphI restriction site (Compound No. 5660).

15 SEQ ID NO:311 nucleic acid sequence for a forward primer with BamHI restriction site (Compound No. 6385).

SEQ ID NO:312 nucleic acid sequence for a forward primer with BglII and NdeI restriction sites (Compound No. 6406).

SEQ ID NO:313 nucleic acid sequence for a forward primer (Compound No. 6470).

SEQ ID NO:314 nucleic acid sequence for a reverse primer (Compound No. 6472).

20 SEQ ID NO:315 nucleic acid sequence for a forward primer with BamHI restriction site (Compound 6473).

SEQ ID NO:316 nucleic acid sequence for a forward primer with BglII and NdeI restriction sites (Compound No. 6474).

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SEQ ID NO:317 nucleic acid sequence for a forward primer (Compound No. 6495).

SEQ ID NO:318 nucleic acid sequence for a reverse primer (Compound No. 6496).

SEQ ID NO:319 nucleic acid sequence for a reverse primer with SphI restriction site (Compound No. 6543).

- 5 SEQ ID NO:320 nucleic acid sequence for a reverse primer with BglII restriction site (Compound No. 6605).

SEQ ID NO:321 nucleic acid sequence for a forward primer with BglII and NdeI restriction sites (Compound No. 6721).

SEQ ID NO:322 nucleic acid sequence for the P4 leader sequence.

- 10 SEQ ID NO:323 nucleic acid sequence for native 2086 leader variant 1.

SEQ ID NO:324 nucleic acid sequence for native 2086 leader variant 2.

SEQ ID NO:325 nucleic acid sequence for native 2086 leader variant 3.

SEQ ID NO:326 nucleic acid sequence for native 2086 leader variant 4.

SEQ ID NO:327 is the amino acid sequence of P4431.

- 15 SEQ ID NO:328 is the amino acid sequence of P5163.

SEQ ID NO:329 is an amino acid sequence according to an embodiment of the present invention.

Detailed Description of the Invention

- 20 A new class of antigens with cross-functional bactericidal activity against *Neisseria meningitidis* serogroup B would obviate the need for a multi-valent PorA approach to immunization against infection. Such an antigen has been unexpectedly identified and is described and claimed herein. The presence of one such antigen was first observed in a complex mixture of soluble outer membrane proteins (sOMPs)

from a meningococcal strain. The bactericidal activity of this antigen was followed through a series of fractionation and protein purification steps until the protein mixture of interest contained just a few proteins. The major proteins in this mixture were identified by N-terminal amino acid sequencing and peptide mapping. The protein of interest exhibiting bactericidal activity was identified as ORF2086 protein, a lipidated protein (also more specifically referred to as LP2086). "ORF2086 protein" refers to a protein encoded by open reading frame 2086 (ORF2086) of *Neisseria species*.

As described herein, new immunogenic composition candidates based on *Neisseria species* ORF2086 protein (also referred to as "2086 protein" or "ORF2086" protein, used interchangeably herein, or P2086 for the non-lipated proteins and LP2086 for the lipidated version of the proteins) isolated from *N. meningitidis* were identified by combining cell fractionation, differential detergent extraction, protein purification, with the preparation of antisera, and a bactericidal activity assay utilizing multiple strains. As an alternative to potential immunogenic compositions and diagnostics disclosed in the references cited above, this invention relates to compositions and methods of treating and/or preventing meningococcal infection through the use of proteins, immunogenic portions thereof and biological equivalents thereof, as well as genes encoding said polypeptides, portions and equivalents, and antibodies that immunospecifically bind to same.

According to an embodiment of the present invention, immunogenic agents based on 2086 protein, including isolated polypeptides, immunogenic portions thereof and/or biological equivalents thereof were unexpectedly identified as immunogenic candidates based on the ability of said agents to exhibit cross-reactivity or non-strain specificity. In particular, candidates were identified that unexpectedly demonstrate the ability to (1) elicit bactericidal antibodies to multiple neisserial and/or gonococcal strains; (2) react with the surface of multiple strains; (3) confer passive protection against a live challenge; and/or (4) prevent colonization. Accordingly, the present invention provides immunogenic compositions comprising said immunogenic agents, including isolated polypeptides, immunogenic portions thereof, and/or biological

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equivalents thereof, as well as methods for using same against infection by *N. meningitidis*. (See Example 1 herein for the methodology used in the identification of the 2086 protein.)

As used herein, the term “non-strain specific” refers to the characteristic of an antigen to elicit an immune response effective against more than one strain of *N. meningitidis* (e.g., heterologous meningococcal strains). The term “cross-reactive” as it is used herein is used interchangeably with the term “non-strain specific”. The term “immunogenic non-strain specific *N. meningitidis* antigen,” as used herein, describes an antigen that can be isolated from *N. meningitidis*, although it can also be isolated from another bacterium (e.g., other neisserial strains, such as gonococcal strains, for example), or prepared using recombinant technology.

The 2086 proteins of the present invention include lipidated and non-lipidated proteins. Further, the present invention also contemplates the use of the immature proteins or preproteins that correspond to each protein as intermediate compounds/compositions.

The present invention also provides antibodies that immunospecifically bind to the foregoing immunogenic agents, according to implementations of the invention. Further, the present invention relates to isolated polynucleotides comprising nucleic acid sequences encoding any of the foregoing. Additionally, the present invention provides compositions and/or immunogenic compositions and their use in preventing, treating and/or diagnosing meningococcal meningitis, in particular serogroup B meningococcal disease, as well as methods for preparing said compositions.

The compositions of the present invention have been shown to be highly immunogenic and capable of eliciting the production of bactericidal antibodies. These antibodies are cross-reactive to serogroup, serotype and serosubtype heterologous meningococcal strains. Accordingly, the present compositions overcome the deficiencies of previous *N. meningitidis* vaccine attempts by exhibiting the ability to elicit bactericidal antibodies to heterologous neisserial strains. Thus, among other advantages, the present invention provides immunogenic compositions

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that can be compounded with fewer components to elicit protection comparable to previously used agents. The compositions or immunogenic agents therein (e.g., polypeptides, immunogenic portions or fragments, and biological equivalents, etc., without limitation) can be used alone or in combination with other antigens or agents to elicit immunological protection from meningococcal infection and disease, as well as to elicit immunological protection from infection and/or disease caused by other pathogens. This simplifies the design of an immunogenic composition for use against meningococcal infection by reducing the number of antigens required for protection against multiple strains. In fact, purified 2086 protein will dramatically and unexpectedly reduce the number of proteins required to provide adequate immunogenic coverage of the strains responsible for meningococcal disease. The 2086 protein can be recombinantly expressed in *E. coli* as a lipoprotein, which is the wild type form of the protein, at levels much higher than in the native meningococci.

Because antibodies directed against the 2086 protein from a single strain were found to kill unrelated (i.e., heterologous) strains, an attempt was made to characterize a large number of heterologous strains for the presence of a "2086 homolog", and to determine the level of sequence conservation. While about 70% of the strains tested by PCR had 2086 homologs that could be amplified using the primers that amplified the original 2086 gene from strain 8529, the remaining approximately 30% were negative by this test. These remaining approximately 30% were found to contain a 2086 homolog that has only about 60% amino acid sequence homology to the original 8529 derived 2086 gene. Other primers were identified that could amplify a 2086 homolog from these approximately 30% of strains. The *N. meningitidis* strains tested have been designated as belonging to Subfamily A or Subfamily B depending on which primer set can amplify a 2086 homolog. The details of these experiments are outlined in Example 5 below.

The presence of a 2086 protein in numerous serosubtypes.

To determine the level of sequence conservation of the 2086 gene between *N. meningitidis* strains, several representatives from Subfamilies A and B were cloned as full length genes and submitted for DNA sequence analysis. Using primers as

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disclosed herein, see, for example, Table IV, twenty four serogroup B meningococcal strains were identified, which express different serosubtype antigens and also express a shared protein, P2086. Examples of these sequences are provided herein and are shown as mature DNA sequences (i.e., all lipoprotein signal sequences have been
5 cleaved at the cysteine residue). See, for example, the amino acid sequences of even numbered SEQ ID NOS: 2-252, without limitation.

Although the 2086 protein is not present in large amounts in wild type strains, it is a target for bactericidal antibodies. These antibodies, unlike those produced in response to the PorAs, are capable of killing strains expressing heterologous
10 serosubtypes.

Antibodies to the 2086 protein also passively protect infant rats from challenge with meningococci. (see Table VII) Recombinant expression of 2086 protein enables the use of 2086 protein as an immunogenic composition for the prevention of meningococcal disease. All of the recent meningococcal immunogenic
15 composition candidates in clinical trials have been complex mixtures or outer membrane protein preparations containing many different proteins. The PorA protein, that provides serosubtype specificity, will require the inclusion of 6 to 9 variants in an immunogenic composition to provide about 70-80% coverage of disease related serosubtypes. In contrast, it is clearly demonstrated herein that antisera to a single
20 2086 protein alone is able to kill representatives of six serosubtypes responsible for about 65% of the disease isolates in western Europe and the United States. Therefore, purified 2086 protein has the potential to reduce the number of proteins required to provide adequate immunogenic composition coverage of the serosubtypes responsible for meningococcal disease.

25 **Proteins, Immunogenic Portions and Biological Equivalents**

The 2086 proteins provided by the present invention are isolated proteins. The term "isolated" means altered by the hand of man from the natural state. If an "isolated" composition or substance occurs in nature, it has been changed or removed from its original environment, or both. For example, a polypeptide or a

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polynucleotide naturally present in a living animal is not “isolated,” but the same polypeptide or polynucleotide separated from the coexisting materials of its natural state is “isolated”, as the term is employed herein. Accordingly, as used herein, the term “isolated protein” encompasses proteins isolated from a natural source and

5 proteins prepared using recombinant technology, as well as such proteins when combined with other antigens and/or additives, such as pharmaceutically acceptable carriers, buffers, adjuvants, etc., for example.

A 2086 protein, immunogenic portion thereof and/or a biological equivalent thereof, according an embodiment of the invention, comprises any of the following

10 amino acid sequences:

ADIGxGLADA (SEQ ID NO:254), wherein x is any amino acid;

IGxGLADALT (SEQ ID NO:255), wherein x is any amino acid;

SLNTGKCLKND (SEQ ID NO:256);

SLNTGKCLKNDKxSRFDF (SEQ ID NO:257, wherein x is any amino acid);

15 SGEFQxYKQ (SEQ ID NO:258), wherein x is any amino acid; or

IEHLKxPE (SEQ ID NO:259), wherein x is any amino acid.

A 2086 Subfamily A protein, immunogenic portion thereof and/or biological equivalent thereof comprises any of the following amino acid sequences, in accordance with an embodiment of the present invention:

20 GGGVAADIGx (SEQ ID NO:260), wherein x is any amino acid;

SGEFQIYKQ (SEQ ID NO:261);

HSAVVALQIE (SEQ ID NO:262);

EKINNPDKID (SEQ ID NO:263);

SLINQRSFLV (SEQ ID NO:264);

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SGLGGEHTAF (SEQ ID NO:265);

GEHTAFNQLP (SEQ ID NO:266);

SFLVSGLGGEH (SEQ ID NO:267);

EKINNPDKIDSLINQRSFLVSGLGGEHTAFNQLP (SEQ ID NO:268);

5 GKAEYHGKAF (SEQ ID NO:269);

YHGKAFSSDD (SEQ ID NO:270);

GKAEYHGKAFSSDD (SEQ ID NO:271);

IEHLKTPEQN (SEQ ID NO: 272);

KTPEQNVELA (SEQ ID NO:273);

10 IEHLKTPEQNVELA (SEQ ID NO:274);

AELKADEKSH (SEQ ID NO:275);

AVILGDTRYG (SEQ ID NO:276);

AELKADEKSHAVILGDTRYG (SEQ ID NO:277); or

EEKGTYHLAL (SEQ ID NO:278).

15 A 2086 Subfamily B protein, immunogenic portion thereof and/or biological equivalent thereof comprises any of the following amino acid sequences, in accordance with an embodiment of the present invention:

LITLESGEFQ (SEQ ID NO:279);

SALTALQTEQ (SEQ ID NO:280);

20 FQVYKQSHSA (SEQ ID NO:281);

LITLESGEFQVYKQSHSALTALQTEQ (SEQ ID NO:282);

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IGDIAGEHTS (SEQ ID NO:283);

EHTSFDKLPK (SEQ ID NO:284);

IGDIAGEHTSFDKLPK (SEQ ID NO:285);

ATYRGTAFGS (SEQ ID NO:286);

5 DDAGGKLTYT (SEQ ID NO:287);

IDFAAKQGHG (SEQ ID NO:288);

KIEHLKSPeL (SEQ ID NO:289);

ATYRGTAFGSDDAGGKLTYTIDFAAKQGHGKIEHLKSPeLNV (SEQ ID
NO: 290);

10 HAVISGSVLY (SEQ ID NO:291);

KGSYSLGIFG (SEQ ID NO:292);

VLYNQDEKGS (SEQ ID NO:293);

HAVISGSVLYNQDEKGSYSLGIFG (SEQ ID NO:294);

AQEVAGSAEV (SEQ ID NO:295);

15 IHHIGLAAKQ (SEQ ID NO:296);

VETANGIHHI (SEQ ID NO:297);

AQEVAGSAEVETANGIHHIGLAAKQ (SEQ ID NO:298); or

VAGSAEVETANGIHHIGLAAKQ (SEQ ID NO:299).

20 The 2086 protein comprises the following consensus sequence and/or
immunogenic portions thereof in accordance with an embodiment of the present
invention.

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2086 Protein Consensus Sequence (SEQ ID NO: 300):

CSSG-----GGGVxADIGxGLADALTxDxKDKxLxSLTLxxSxxxNxxLxLxAQGA
 EKTxxxGD---SLNTGKLKNDKxSRFDFxxxIxVDGxxITLxSGEFQxYKQxHSAxx
 ALQxExxxxxxxxxxxxxRxFxxxxxGEHTxFxxLPxx-xAxYxGxAFxSDDxxGxLxYx
 5 IDFxKQGxGxIEHLKxPExNVxLAxxxxKxDEKxHAVIxGxxxYxxxEKGxYxLxxx
 GxxAQExAGxAxVxxxxxxHxIxxAxKQ

In the foregoing consensus sequence, the “x” represents any amino acid, the
 region from amino acid position 5 to amino acid position 9 is any of 0 to 5 amino
 acids, the region from amino acid position 67 to amino acid position 69 is any of 0 to
 10 3 amino acids, and amino acid position 156 is any of 0 to 1 amino acid. The region
 from amino acid position 5 to amino acid position 9 preferably comprises 0, 4 or 5
 amino acids. The region from amino acid position 67 to amino acid position 69
 preferably comprises 0 or 3 amino acids. It should be particularly noted that this
 consensus sequence illustrates the high variability of the 2086 proteins. By way of
 15 theory, without intending to be bound thereto, it is believed that this high variability
 provides the advantageous and unexpected cross-reactivity.

According to an implementation of the present invention, the 2086 proteins are
 characterized as being immunogenic, nonpathogenic and non-strain specific.
 Moreover, according to a further implementation of the present invention, these
 20 proteins unexpectedly exhibit immunogenicity while being about 2% to about 40%
 nonconserved.

As used herein, the term “nonconserved” refers to the number of amino acids
 that may undergo insertions, substitution and/or deletions as a percentage of the total
 number of amino acids in a protein. For example, if a protein is 40% nonconserved
 25 and has, for example, 263 amino acids, then there are 105 amino acid positions in the
 protein at which amino acids may undergo substitution. Likewise, if a protein is 10%
 nonconserved and has, for example, about 280 amino acids, then there are 28 amino
 acid positions at which amino acids may undergo substitution. The 2086 proteins
 may also undergo deletion of amino acid residues without compromising the
 30 immunogenicity of the proteins.

Further, the 2086 proteins may be divided into subfamilies based upon homology at various regions. For example, without intending to be limited thereto, the consensus sequences for two such subfamilies, Subfamily A and Subfamily B, are provided below:

5

2086 Subfamily A sequence (SEQ ID 301)

CSSG---GGGVAADIGxGLADALTxPxDxDKxLxSLTLxxSxxxNxxLxLxAQGA
 EKTxxxGD---SLNTGKLKNDKxSRFDFxxxIxVDGQxITLxSGEFQIYKQxHSAVV
 10 ALQIEKINNPDKIDSLINQRSFLVSGLGGEHTAFNQLPxGKAEYHGKAFSSDDx
 xGxLxYxIDFxxKQGxGxIEHLKTPEQNVELAxAELKADEKSHAVILGDTRYGxE
 EKGTYHLALxGDRAQEIAGxATVKIxEKVHEIxIAxKQ

The reference “x” is any amino acid.

15

The region from amino acid position 5 to amino acid position 8 is any of 0 to 4 amino acids.

The region from amino acid position 66 to amino acid position 68 is any of 0 to 3 amino acids.

20 The region from amino acid position 5 to amino acid position 8 preferably comprises 0 or 4 amino acids. The region from amino acid position 66 to amino acid position 68 preferably comprises 0 or 3 amino acids.

2086 Subfamily B (SEQ ID 302)

25 CSSGGGG-----VxADIGxGLADALTAPLDHKDKxLxSLTLxxSxxxNxxLxLxAQ
 GAEKTYGNGDSLNTGKLKNDKVSRLFDFIRQIEVDGxLITLESGEFQVYKQSHS
 ALTALQTEQxQDxExSxKMVAKRxFxIGDIAGEHTSFDKLPKxxxATYRGTAFGS
 DDAGGKLTYTIDFAAKQGHGKIEHLKSPELNVxLAxxYIKPDEKxHAVISGSVL
 YNQDEKGSYSLGIFGxxAQEVAGSAEVETANGIHHIGLAAKQ

30

The reference “x” is any amino acid.

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The region from amino acid position 8 to amino acid position 12 is any of 0 to 5 amino acids.

The region from amino acid position 8 to amino acid position 12 preferably comprises 0 or 5 amino acids.

5 According to implementations of the present invention, the 2086 protein subfamilies may be further subdivided into clusters. For example, according to an implementation of the present invention, the following clusters are provided: even numbered SEQ ID NOS:2-12; even numbered SEQ ID NOS:14-24; even numbered SEQ ID NOS:26-42; even numbered SEQ ID NOS:50-60; even numbered SEQ ID NOS:62-108; even numbered SEQ ID NOS:110-138; even numbered SEQ ID NOS:140-156; even numbered SEQ ID NOS:158-174; and even numbered SEQ ID NOS: 224-252.

15 A polypeptide sequence of the invention may be identical to the reference sequence of even numbered SEQ ID NOS: 2-252, that is, 100% identical, or it may include a number of amino acid alterations as compared to the reference sequence such that the % identity is less than 100%. Such alterations include at least one amino acid deletion, substitution, including conservative and non-conservative substitution, or insertion. The alterations may occur at the amino- or carboxy-terminal positions of the reference polypeptide sequence or anywhere between those terminal positions, interspersed either individually among the amino acids in the reference amino acid sequence or in one or more contiguous groups within the reference amino acid sequence.

25 Thus, the invention also provides proteins having sequence identity to the amino acid sequences contained in the Sequence Listing (i.e., even numbered SEQ ID NOS: 2-252). Depending on the particular sequence, the degree of sequence identity is preferably greater than 60% (e.g., 60%, 70%, 80%, 90%, 95%, 97%, 99%, 99.9% or more). These homologous proteins include mutants and allelic variants.

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In preferred embodiments of the invention, the 2086 proteins or other 2086 polypeptides (e.g., immunological portions and biological equivalents) generate bactericidal antibodies to homologous and at least one heterologous strain of meningococci. Specifically, the antibodies to the 2086 polypeptides passively protect
5 infant rats from challenge, such as intranasal, with meningococci. In further preferred embodiments, the 2086 polypeptides exhibit such protection for infants rats for homologous strains and at least one heterologous strain. The polypeptide may be selected from the Sequence Summary above, as set forth in the even numbered SEQ ID NOS: 2-252, or the polypeptide may be any immunological fragment or biological
10 equivalent of the listed polypeptides. Preferably, the polypeptide is selected from any of the even numbered SEQ ID NOS: 2-252 in the Sequence Summary above.

This invention also relates to allelic or other variants of the 2086 polypeptides, which are biological equivalents. Suitable biological equivalents will exhibit the ability to (1) elicit bactericidal antibodies to homologous strains and at least one
15 heterologous neisserial strain and/or gonococcal strain; (2) react with the surface of homologous strains and at least one heterologous neisserial and/or gonococcal strain; (3) confer passive protection against a live challenge; and/or (4) prevent colonization.

Suitable biological equivalents have at least about 60%, preferably at least about 70%, more preferably at least about 75%, even more preferably about 80%,
20 even more preferably about 85%, even more preferably about 90%, even more preferably 95 % or even more preferably 98%, or even more preferably 99% similarity to one of the 2086 polypeptides specified herein (i.e., the even numbered SEQ ID NOS: 2-252), provided the equivalent is capable of eliciting substantially the same immunogenic properties as one of the 2086 proteins of this invention.

25 Alternatively, the biological equivalents have substantially the same immunogenic properties of one of the 2086 protein in the even numbered SEQ ID NOS: 2-252. According to embodiments of the present invention, the biological equivalents have the same immunogenic properties as the even numbered SEQ ID NOS 2-252.

The biological equivalents are obtained by generating variants and modifications to the proteins of this invention. These variants and modifications to the proteins are obtained by altering the amino acid sequences by insertion, deletion or substitution of one or more amino acids. The amino acid sequence is modified, for example by substitution in order to create a polypeptide having substantially the same or improved qualities. A preferred means of introducing alterations comprises making predetermined mutations of the nucleic acid sequence of the polypeptide by site-directed mutagenesis.

Modifications and changes can be made in the structure of a polypeptide of the present invention and still obtain a molecule having *N. meningitidis* immunogenicity. For example, without limitation, certain amino acids can be substituted for other amino acids, including nonconserved and conserved substitution, in a sequence without appreciable loss of immunogenicity. Because it is the interactive capacity and nature of a polypeptide that defines that polypeptide's biological functional activity, a number of amino acid sequence substitutions can be made in a polypeptide sequence (or, of course, its underlying DNA coding sequence) and nevertheless obtain a polypeptide with like properties. The present invention contemplates any changes to the structure of the polypeptides herein, as well as the nucleic acid sequences encoding said polypeptides, wherein the polypeptide retains immunogenicity. A person of ordinary skill in the art would be readily able to modify the disclosed polypeptides and polynucleotides accordingly, based upon the guidance provided herein.

For example, certain variable regions have been identified where substitution or deletion is permissible. The 2086 consensus sequence, as previously discussed, shows conserved and nonconserved regions of the 2086 family of proteins according to an implementation of the present invention.

In making such changes, any techniques known to persons of skill in the art may be utilized. For example, without intending to be limited thereto, the hydropathic index of amino acids can be considered. The importance of the hydropathic amino

acid index in conferring interactive biologic function on a polypeptide is generally understood in the art. Kyte *et al.* 1982. *J. Mol. Bio.* 157:105-132.

Substitution of like amino acids can also be made on the basis of hydrophilicity, particularly where the biological functional equivalent polypeptide or peptide thereby created is intended for use in immunological embodiments. U.S. Pat. No. 4,554,101, incorporated herein by reference, states that the greatest local average hydrophilicity of a polypeptide, as governed by the hydrophilicity of its adjacent amino acids, correlates with its immunogenicity, *i.e.* with a biological property of the polypeptide.

Biological equivalents of a polypeptide can also be prepared using site-specific mutagenesis. Site-specific mutagenesis is a technique useful in the preparation of second generation polypeptides, or biologically functional equivalent polypeptides or peptides, derived from the sequences thereof, through specific mutagenesis of the underlying DNA. Such changes can be desirable where amino acid substitutions are desirable. The technique further provides a ready ability to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the DNA. Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Typically, a primer of about 17 to 25 nucleotides in length is preferred, with about 5 to 10 residues on both sides of the junction of the sequence being altered.

In general, the technique of site-specific mutagenesis is well known in the art. As will be appreciated, the technique typically employs a phage vector which can exist in both a single stranded and double stranded form. Typically, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector which includes within its sequence a DNA sequence which encodes all or a portion of the *N. meningitidis* polypeptide sequence selected. An oligonucleotide

primer bearing the desired mutated sequence is prepared (*e.g.*, synthetically). This primer is then annealed to the single-stranded vector, and extended by the use of enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells such as *E. coli* cells and clones are selected which include recombinant vectors bearing the mutation. Commercially available kits come with all the reagents necessary, except the oligonucleotide primers.

2086 polypeptides include any protein or polypeptide comprising substantial sequence similarity and/or biological equivalence to a 2086 protein having an amino acid sequence from one of the even numbered SEQ ID NOS 2-252. In addition, a 2086 polypeptide of the invention is not limited to a particular source. Thus, the invention provides for the general detection and isolation of the polypeptides from a variety of sources. Also, the 2086 polypeptides can be prepared recombinantly, as is well within the skill in the art, based upon the guidance provided herein, or in any other synthetic manner, as known in the art.

It is contemplated in the present invention, that a 2086 polypeptide may advantageously be cleaved into fragments for use in further structural or functional analysis, or in the generation of reagents such as 2086-related polypeptides and 2086-specific antibodies. This can be accomplished by treating purified or unpurified *N. meningitidis* polypeptides with a peptidase such as endoproteinase glu-C (Boehringer, Indianapolis, IN). Treatment with CNBr is another method by which peptide fragments may be produced from natural *N. meningitidis* 2086 polypeptides.

Recombinant techniques also can be used to produce specific fragments of a 2086 protein.

“Variant” as the term is used herein, is a polynucleotide or polypeptide that differs from a reference polynucleotide or polypeptide respectively, but retains essential properties. A typical variant of a polynucleotide differs in nucleotide sequence from another, reference polynucleotide. Changes in the nucleotide sequence

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of the variant may or may not alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes may result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference sequence, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from another, reference polypeptide. Generally, differences are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions, identical (*i.e.*, biologically equivalent). A variant and reference polypeptide may differ in amino acid sequence by one or more substitutions, additions, deletions in any combination. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. A variant of a polynucleotide or polypeptide may be a naturally occurring such as an allelic variant, or it may be a variant that is not known to occur naturally. Non-naturally occurring variants of polynucleotides and polypeptides may be made by mutagenesis techniques or by direct synthesis.

“Identity,” as known in the art, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, “identity” also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. “Identity” and “similarity” can be readily calculated by known methods, including but not limited to those described in Computational Molecular Biology, Lesk, A. M., ed., Oxford University Press, New York, 1988; Biocomputing: Informatics and Genome Projects, Smith, D. W., ed., Academic Press, New York, 1993; Computer Analysis of Sequence Data, Part I, Griffin, A. M., and Griffin, H. G., eds., Humana Press, New Jersey, 1994; Sequence Analysis in Molecular Biology, von Heinje, G., Academic Press, 1987; and Sequence Analysis Primer, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D., *SIAM J. Applied Math.*, 48:1073 (1988). Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in publicly available computer programs. Preferred computer program methods to determine identity and similarity between two sequences include,

but are not limited to, the GCG program package (Devereux, J., *et al* 1984), BLASTP, BLASTN, and FASTA (Altschul, S. F., *et al.*, 1990). The BLASTX program is publicly available from NCBI and other sources (BLAST Manual, Altschul, S., *et al.*, NCBI NLM NIH Bethesda, Md. 20894; Altschul, S., *et al.*, 1990). The well known
 5 Smith Waterman algorithm may also be used to determine identity.

By way of example, without intending to be limited thereto, an amino acid sequence of the present invention may be identical to the reference sequences, even numbered SEQ ID NOS: 2-252; that is be 100% identical, or it may include a number of amino acid alterations as compared to the reference sequence such that the %
 10 identity is less than 100%. Such alterations are selected from the group consisting of at least one amino acid deletion, substitution, including conservative and non-conservative substitution, or insertion, and wherein said alterations may occur at the amino- or carboxy-terminal positions of the reference polypeptide sequence or anywhere between those terminal positions, interspersed either individually among
 15 the amino acids in the reference sequence or in one or more contiguous groups within the reference sequence. The number of amino acid alterations for a given % identity is determined by multiplying the total number of amino acids in SEQ ID NOS:2-252 by the numerical percent of the respective percent identity (divided by 100) and then subtracting that product from said total number of amino acids in any of SEQ ID
 20 NOS:2-252, or:

$$n_a = x_a - (x_a \bullet y),$$

wherein n_a is the number of amino acid alterations, x_a is the total number of amino acids in SEQ ID NOS:2-252, and y is, for instance 0.70 for 70%, 0.80 for 80%, 0.85 for 85% etc., and wherein any non-integer product of $x_{\text{sub}.a}$ and y is rounded down
 25 to the nearest integer prior to subtracting it from x_a .

In preferred embodiments, the polypeptide above is selected from the proteins set forth in the even numbered SEQ ID NOS 2-252, such as mature processed form of a 2086 protein. The 2086 proteins or equivalents, etc. may be lipidated or non-lipidated.

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ORF 2086 is expressible in *E. coli* with the native ORF 2086 signal sequence. However, it is desirable to find means to improve the expression of proteins. According to an embodiment of the present invention, a leader sequence produces a lipidated form of the protein. For example, the following describes the use of the
5 signal sequence of the nontypable *Haemophilus influenzae* P4 protein to enhance expression.

The processing of bacterial lipoproteins begins with the synthesis of a precursor or prolipoprotein containing a signal sequence, which in turn contains a consensus lipoprotein processing/modification site. This prolipoprotein initially
10 passes through the common Sec system on the inner membrane of Gram negative bacteria or on the membrane in Gram positive bacteria. Once placed in the membrane by the Sec system, the prolipoprotein is cleaved by signal peptidase II at the consensus site and the exposed N-terminal cysteine residue is glycerated and acylated. Hayashi et al. 1990. Lipoproteins in bacteria. *J. Bioenerg. Biomembr.* Jun;
15 22(3):451-71; Oudega et al. 1993. *Escherichia coli* SecB, SecA, and SecY proteins are required for expression and membrane insertion of the bacteriocin release protein, a small lipoprotein. *J. Bacteriol.* Mar;175(5):1543-7; Sankaran et al. 1995. Modification of bacterial lipoproteins. *Methods Enzymol.* 250:683-97.

In Gram negative bacteria, transport of the lipidated protein to the outer
20 membrane is mediated by a unique ABC transporter system with membrane specificity depending on a sorting signal at position 2 of the lipoprotein. Yakushi et al. 2000. A new ABC transporter mediating the detachment of lipid modified proteins from membranes. *Nat Cell Biol.* Apr;2(4):212-8.

Fusion with bacterial lipoproteins and their signal sequences has been used to
25 display recombinant proteins on the surface of bacteria. U.S. Patent Numbers 5,583,038 and 6,130,085. Exchanging lipoprotein signal sequences can increase the production of the lipoprotein. De et al. 2000. Purification and characterization of *Streptococcus pneumoniae* palmitoylated pneumococcal surface adhesin A expressed in *Escherichia coli*. *Vaccine.* Mar 6;18(17):1811-21.

Bacterial lipidation of proteins is known to increase or modify the immunological response to proteins. Erdile et al. 1993. Role of attached lipid in immunogenicity of *Borrelia burgdorferi* OspA. *Infect. Immun.* Jan;61(1):81-90; Snapper et al. 1995. Bacterial lipoproteins may substitute for cytokines in the humoral immune response to T cell-independent type II antigens. *J. Immunol.* Dec 15;155(12):5582-9. However, bacterial lipoprotein expression can be complicated by the stringency of the processing. Pollitt et al. 1986. Effect of amino acid substitutions at the signal peptide cleavage site of the *Escherichia coli* major outer membrane lipoprotein. *J. Biol. Chem.* Feb 5; 261(4):1835-7; Lunn et al. 1987. Effects of prolipoprotein signal peptide mutations on secretion of hybrid prolipo-beta-lactamase in *Escherichia coli*. *J. Biol. Chem.* Jun 15;262(17):8318-24; Klein et al. 1988. Distinctive properties of signal sequences from bacterial lipoproteins. *Protein Eng.* Apr; 2(1):15-20. Bacterial lipoprotein expression is also complicated by other problems such as toxicity and low expression levels. Gomez et al. 1994. Nucleotide The *Bacillus subtilis* lipoprotein LplA causes cell lysis when expressed in *Escherichia coli*. *Microbiology.* Aug;140 (Pt 8):1839-45; Hansson et al. 1995. Expression of truncated and full-length forms of the Lyme disease *Borrelia* outer surface protein A in *Escherichia coli*. *Protein Expr. Purif.* Feb; 6(1):15-24; Yakushi et al. 1997. Lethality of the covalent linkage between mislocalized major outer membrane lipoprotein and the peptidoglycan of *Escherichia coli*. *J. Bacteriol.* May; 179(9):2857-62.

The nontypable *Haemophilus influenzae* bacterium expresses a lipoprotein designated P4 (also known as protein "e"). The recombinant form of the P4 protein is highly expressed in *E. coli* using the native P4 signal sequence. U.S. Patent Number 5,955,580. When the native P4 signal sequence is substituted for the native ORF 2086 signal sequence in an expression vector in *E. coli*, the level of expression of ORF2086 is increased.

This concept of using the heterologous P4 signal sequence to increase expression is extendible to other bacterial lipoproteins. In particular, analysis of bacterial genomes leads to the identification of many ORFs as being of possible

interest. Attempting to express each ORF with its native signal sequence in a heterologous host cell, such as *E. coli*, gives rise to a variety of problems inherent in using a variety of signal sequences, including stability, compatibility and so forth. To minimize these problems, the P4 signal sequence is used to express each ORF of interest. As described above, the P4 signal sequence improves the expression of the heterologous 2086 ORF. An expression vector is constructed by deleting the native signal sequence of the ORF of interest, and ligating the P4 signal sequence to the ORF. A suitable host cell is then transformed, transfected or infected with the expression vector, and expression of the ORF is increased in comparison to expression using the native signal sequence of the ORF.

The non-lipidated form is produced by a protein lacking the original leader sequence or a by a leader sequence which is replaced with a portion of sequence that does not specify a site for fatty acid acylation in a host cell.

The various forms of the 2086 proteins of this invention are referred to herein as “2086” protein, unless otherwise specifically noted. Also “2086 polypeptide” refers to the 2086 proteins as well as immunogenic portions or biological equivalents thereof as noted above, unless otherwise noted.

The full length isolated and purified *N. meningitidis* 2086 protein has an apparent molecular weight of about 28 to 35 kDa as measured on a 10 % to 20% gradient SDS polyacrylamide gel (SDS-PAGE). More specifically, this protein has a molecular weight of about 26,000 to 30,000 daltons as measured by mass spectrometry.

Preferably, the 2086 polypeptides and nucleic acids encoding such polypeptides are used for preventing or ameliorating infection caused by *N. meningitidis* and/or other species.

Antibodies

The proteins of the invention, including the amino acid sequences of SEQ ID NOS: 2-252, their fragments, and analogs thereof, or cells expressing them, are also

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used as immunogens to produce antibodies immunospecific for the polypeptides of the invention. The invention includes antibodies to immunospecific polypeptides and the use of such antibodies to detect the presence of *N. meningitidis*, provide passive protection or measure the quantity or concentration of the polypeptides in a cell, a cell
5 or tissue extract, or a biological fluid.

The antibodies of the invention include polyclonal antibodies, monoclonal antibodies, chimeric antibodies, and anti-idiotypic antibodies. Polyclonal antibodies are heterogeneous populations of antibody molecules derived from the sera of animals immunized with an antigen. Monoclonal antibodies are a substantially homogeneous
10 population of antibodies to specific antigens. Monoclonal antibodies may be obtained by methods known to those skilled in the art, e.g., Kohler and Milstein, 1975, *Nature* 256:495-497 and U.S. Patent Number 4,376,110. Such antibodies may be of any immunoglobulin class including IgG, IgM, IgE, IgA, GILD and any subclass thereof.

Chimeric antibodies are molecules, different portions of which are derived
15 from different animal species, such as those having variable region derived from a murine monoclonal antibody and a human immunoglobulin constant region. Chimeric antibodies and methods for their production are known in the art (Cabilly *et al.*, 1984, *Proc. Natl. Acad. Sci. USA* 81:3273-3277; Morrison *et al.*, 1984, *Proc. Natl. Acad. Sci. USA* 81:6851-6855; Boulianne *et al.*, 1984, *Nature* 312:643-646;
20 Cabilly *et al.*, European Patent Application 125023 (published November 14, 1984); Taniguchi *et al.*, European Patent Application 171496 (published February 19, 1985); Morrison *et al.*, European Patent Application 173494 (published March 5, 1986); Neuberger *et al.*, PCT Application WO 86/01533 (published March 13, 1986); Kudo *et al.*, European Patent Application 184187 (published June 11, 1986); Morrison *et al.*,
25 *et al.*, European Patent Application 173494 (published March 5, 1986); Sahagan *et al.*, 1986, *J. Immunol.* 137:1066-1074; Robinson *et al.*, PCT/US86/02269 (published May 7, 1987); Liu *et al.*, 1987, *Proc. Natl. Acad. Sci. USA* 84:3439-3443; Sun *et al.*, 1987, *Proc. Natl. Acad. Sci. USA* 84:214-218; Better *et al.*, 1988, *Science* 240:1041-1043). These references are hereby incorporated by reference in their entirety.

An anti-idiotypic (anti-Id) antibody is an antibody which recognizes unique determinants generally associated with the antigen-binding site of an antibody. An anti-Id antibody is prepared by immunizing an animal of the same species and genetic type (e.g., mouse strain) as the source of the monoclonal antibody with the
5 monoclonal antibody to which an anti-Id is being prepared. The immunized animal will recognize and respond to the idiotypic determinants of the immunizing antibody by producing an antibody to these isotypic determinants (the anti-Id antibody).

Accordingly, monoclonal antibodies generated against the polypeptides of the present invention may be used to induce anti-Id antibodies in suitable animals. Spleen
10 cells from such immunized mice can be used to produce anti-Id hybridomas secreting anti-Id monoclonal antibodies. Further, the anti-Id antibodies can be coupled to a carrier such as keyhole limpet hemocyanin (KLH) and used to immunize additional BALB/c mice. Sera from these mice will contain anti-anti-Id antibodies that have the binding properties of the final mAb specific for an R-PTPase epitope. The anti-Id
15 antibodies thus have their idiotypic epitopes, or "idiotopes" structurally similar to the epitope being evaluated, such as *Streptococcus pyogenes* polypeptides.

The term "antibody" is also meant to include both intact molecules as well as fragments such as Fab which are capable of binding antigen. Fab fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have
20 less non-specific tissue binding than an intact antibody (Wahl *et al.*, 1983, *J. Nucl. Med.* 24:316-325). It will be appreciated that Fab and other fragments of the antibodies useful in the present invention may be used for the detection and quantitation of *N. meningitidis* polypeptides according to the methods for intact antibody molecules.

25 The antibodies of this invention, such as anti-idiotypic ("anti-Id") antibodies, can be employed in a method for the treatment or prevention of *Neisseria* infection in mammalian hosts, which comprises administration of an immunologically effective amount of antibody, specific for a polypeptide as described above. The anti-Id antibody may also be used as an "immunogen" to induce an immune response in yet
30 another animal, producing a so-called anti-anti-Id antibody. The anti-anti-Id may be

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epitopically identical to the original mAb which induced the anti-Id. Thus, by using antibodies to the idiotypic determinants of a mAb, it is possible to identify other clones expressing antibodies of identical specificity.

5 The antibodies are used in a variety of ways, e.g., for confirmation that a protein is expressed, or to confirm where a protein is expressed. Labeled antibody (e.g., fluorescent labeling for FACS) can be incubated with intact bacteria and the presence of the label on the bacterial surface confirms the location of the protein, for instance.

10 Antibodies generated against the polypeptides of the invention can be obtained by administering the polypeptides or epitope-bearing fragments, analogs, or cells to an animal using routine protocols. For preparing monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures are used.

Polynucleotides

15 As with the proteins of the present invention, a polynucleotide of the present invention may comprise a nucleic acid sequence that is identical to any of the reference sequences of odd numbered SEQ ID NOS:1-253, that is be 100% identical, or it may include up to a number of nucleotide alterations as compared to the reference sequence. Such alterations are selected from the group consisting of at least
20 one nucleotide deletion, substitution, including transition and transversion, or insertion, and wherein said alterations may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among the nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence. The number of
25 nucleotide alterations is determined by multiplying the total number of nucleotides in any of odd numbered SEQ ID NOS:1-253 by the numerical percent of the respective percent identity (divided by 100) and subtracting that product from said total number of nucleotides in said sequence.

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By way of example, without intending to be limited thereto, an isolated *N. meningitidis* polynucleotide comprising a polynucleotide sequence that has at least 70% identity to any nucleic acid sequence of SEQ ID NOS:1-253; a degenerate variant thereof or a fragment thereof, wherein the polynucleotide sequence may

5 include up to n_n nucleic acid alterations over the entire polynucleotide region of the nucleic acid sequence of SEQ ID NOS:1-253, wherein n_n is the maximum number of alterations and is calculated by the formula:

$$n_n = x_n - (x_n \cdot y),$$

in which x_n is the total number of nucleic acids of any of SEQ ID NOS:1-253 and y has a value of 0.70, wherein any non-integer product of x_n and y is rounded down to the nearest integer prior to subtracting such product from x_n . Of course, y may also have a value of 0.80 for 80%, 0.85 for 85%, 0.90 for 90% 0.95 for 95%, *etc.*

Alterations of a polynucleotide sequence encoding the polypeptides comprising amino acid sequences of any of SEQ ID NOS:2-252 may create nonsense, missense or

15 frameshift mutations in this coding sequence and thereby alter the polypeptide encoded by the polynucleotide following such alterations.

Certain embodiments of the present invention relate to polynucleotides (herein referred to as the “2086 polynucleotides” or “ORF2086 polynucleotides”) which encode the 2086 proteins and antibodies made against the 2086 proteins. In preferred

20 embodiments, an isolated polynucleotide of the present invention is a polynucleotide comprising a nucleotide sequence having at least about 95% identity to a nucleotide sequence chosen from one of the odd numbered SEQ ID NO: 1 and SEQ ID NOS: 253, a degenerate variant thereof, or a fragment thereof. As defined herein, a

“degenerate variant” is defined as a polynucleotide that differs from the nucleotide

25 sequence shown in the odd numbered SEQ ID NOS:1 and SEQ ID NOS:253 (and fragments thereof) due to degeneracy of the genetic code, but still encodes the same 2086 protein (*i.e.*, the even numbered SEQ ID NOS: 2-252) as that encoded by the nucleotide sequence shown in the odd numbered SEQ ID NOS: 1-253.

In other embodiments, the polynucleotide is a complement to a nucleotide sequence chosen from one of the odd numbered SEQ ID NOS: 1-253, a degenerate variant thereof, or a fragment thereof. In yet other embodiments, the polynucleotide is selected from the group consisting of DNA, chromosomal DNA, cDNA and RNA and may further comprises heterologous nucleotides. In another embodiment, an isolated polynucleotide hybridizes to a nucleotide sequence chosen from one of SEQ ID NOS: 1 -253, a complement thereof, a degenerate variant thereof, or a fragment thereof, under high stringency hybridization conditions. In yet other embodiments, the polynucleotide hybridizes under intermediate stringency hybridization conditions.

It will be appreciated that the 2086 polynucleotides may be obtained from natural, synthetic or semi-synthetic sources; furthermore, the nucleotide sequence may be a naturally occurring sequence, or it may be related by mutation, including single or multiple base substitutions, deletions, insertions and inversions, to such a naturally occurring sequence, provided always that the nucleic acid molecule comprising such a sequence is capable of being expressed as 2086 immunogenic polypeptide as described above. The nucleic acid molecule may be RNA, DNA, single stranded or double stranded, linear or covalently closed circular form. The nucleotide sequence may have expression control sequences positioned adjacent to it, such control sequences usually being derived from a heterologous source. Generally, recombinant expression of the nucleic acid sequence of this invention will use a stop codon sequence, such as TAA, at the end of the nucleic acid sequence.

The invention also includes polynucleotides capable of hybridizing under reduced stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the Stringency Conditions Table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

STRINGENCY CONDITIONS - TABLE I

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) ^I	Hybridization Temperature and Buffer ^H	Wash Temperature and Buffer ^H
A	DNA:DNA	> 50	65EC; 1xSSC -or- 42EC; 1xSSC, 50% formamide	65EC; 0.3xSSC
B	DNA:DNA	< 50	T _B ; 1xSSC	T _B ; 1xSSC
C	DNA:RNA	> 50	67EC; 1xSSC -or- 45EC; 1xSSC, 50% formamide	67EC; 0.3xSSC
D	DNA:RNA	< 50	T _D ; 1xSSC	T _D ; 1xSSC
E	RNA:RNA	> 50	70EC; 1xSSC -or- 50EC; 1xSSC, 50% formamide	70EC; 0.3xSSC
F	RNA:RNA	< 50	T _F ; 1xSSC	T _F ; 1xSSC
G	DNA:DNA	> 50	65EC; 4xSSC -or- 42EC; 4xSSC, 50% formamide	65EC; 1xSSC
H	DNA:DNA	< 50	T _H ; 4xSSC	T _H ; 4xSSC
I	DNA:RNA	> 50	67EC; 4xSSC -or- 45EC; 4xSSC, 50% formamide	67EC; 1xSSC
J	DNA:RNA	< 50	T _J ; 4xSSC	T _J ; 4xSSC
K	RNA:RNA	> 50	70EC; 4xSSC -or- 50EC; 4xSSC, 50% formamide	67EC; 1xSSC
L	RNA:RNA	< 50	T _L ; 2xSSC	T _L ; 2xSSC
M	DNA:DNA	> 50	50EC; 4xSSC -or- 40EC; 6xSSC, 50% formamide	50EC; 2xSSC
N	DNA:DNA	< 50	T _N ; 6xSSC	T _N ; 6xSSC
O	DNA:RNA	> 50	55EC; 4xSSC -or- 42EC; 6xSSC, 50% formamide	55EC; 2xSSC
P	DNA:RNA	< 50	T _P ; 6xSSC	T _P ; 6xSSC
Q	RNA:RNA	> 50	60EC; 4xSSC -or- 45EC; 6xSSC, 50% formamide	60EC; 2xSSC
R	RNA:RNA	< 50	T _R ; 4xSSC	T _R ; 4xSSC

bp^I: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the

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hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarities.

- 5 buffer^H: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

- T_B through T_R: The hybridization temperature for hybrids anticipated to be
10 less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(EC) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(EC) = 81.5 + 16.6(log₁₀[Na⁺]) + 0.41(%G+C) - (600/N), where N is the number of bases in the
15 hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1xSSC = 0.165 M).

- Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor,
20 NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel *et al.*, eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

- The invention also provides polynucleotides that are fully complementary to these polynucleotides and also provides antisense sequences. The antisense
25 sequences of the invention, also referred to as antisense oligonucleotides, include both internally generated and externally administered sequences that block expression of polynucleotides encoding the polypeptides of the invention. The antisense sequences of the invention comprise, for example, about 15-20 base pairs. The antisense sequences can be designed, for example, to inhibit transcription by preventing

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promoter binding to an upstream nontranslated sequence or by preventing translation of a transcript encoding a polypeptide of the invention by preventing the ribosome from binding.

5 The polynucleotides of the invention are prepared in many ways (e.g., by chemical synthesis, from DNA libraries, from the organism itself) and can take various forms (e.g., single-stranded, double-stranded, vectors, probes, primers). The term “polynucleotide” includes DNA and RNA, and also their analogs, such as those containing modified backbones.

10 According to further implementations of the present invention, the polynucleotides of the present invention comprise a DNA library, such as a cDNA library.

Fusion Proteins

The present invention also relates to fusion proteins. A “fusion protein” refers to a protein encoded by two, often unrelated, fused genes or fragments thereof. For
15 example, fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another immunogenic protein or part thereof. In many cases, employing an immunoglobulin Fc region as a part of a fusion protein is advantageous for use in therapy and diagnosis resulting in, for example, improved pharmacokinetic properties (*see, e.g.*, EP 0 232 262 A1). On the other
20 hand, for some uses it would be desirable to be able to delete the Fc part after the fusion protein has been expressed, detected and purified. The 2086 polynucleotides of the invention are used for the recombinant production of polypeptides of the present invention, the polynucleotide may include the coding sequence for the mature polypeptide, by itself, or the coding sequence for the mature polypeptide in reading
25 frame with other coding sequences, such as those encoding a leader or secretory sequence, a pre-, or pro- or prepro- protein sequence, or other fusion peptide portions. For example, a marker sequence which facilitates purification of a 2086 polypeptide or fused polypeptide can be encoded (*see Gentz et al.*, 1989, incorporated herein by reference in its entirety). Thus, contemplated in an implementation of the present

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invention is the preparation of polynucleotides encoding fusion polypeptides permitting His-tag purification of expression products. The polynucleotide may also contain non-coding 5' and 3' sequences, such as transcribed, non-translated sequences, splicing and polyadenylation signals. Such a fused polypeptide can be
5 produced by a host cell transformed/transfected or infected or infected with a recombinant DNA cloning vehicle as described below and it can be subsequently isolated from the host cell to provide the fused polypeptide substantially free of other host cell proteins.

Immunogenic Compositions

10 One aspect of the present invention provides immunogenic compositions which comprise at least one 2086 proteins or a nucleic acid encoding said proteins. The foregoing have the ability to (1) elicit bactericidal antibodies to multiple strains; (2) react with the surface of multiple strains; (3) confer passive protection against a live challenge; and/or (4) prevent colonization.

15 The formulation of such immunogenic compositions is well known to persons skilled in this field. Immunogenic compositions of the invention preferably include a pharmaceutically acceptable carrier. Suitable pharmaceutically acceptable carriers and/or diluents include any and all conventional solvents, dispersion media, fillers, solid carriers, aqueous solutions, coatings, antibacterial and antifungal agents, isotonic
20 and absorption delaying agents, and the like. Suitable pharmaceutically acceptable carriers include, for example, one or more of water, saline, phosphate buffered saline, dextrose, glycerol, ethanol and the like, as well as combinations thereof. Pharmaceutically acceptable carriers may further comprise minor amounts of auxiliary substances such as wetting or emulsifying agents, preservatives or buffers,
25 which enhance the shelf life or effectiveness of the antibody. The preparation and use of pharmaceutically acceptable carriers is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, use thereof in the immunogenic compositions of the present invention is contemplated.

Such immunogenic compositions can be administered parenterally, e.g., by injection, either subcutaneously or intramuscularly, as well as orally or intranasally. Methods for intramuscular immunization are described by Wolff *et al.* and by Sedegah *et al.* Other modes of administration employ oral formulations, pulmonary
5 formulations, suppositories, and transdermal applications, for example, without limitation. Oral formulations, for example, include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, and the like, without limitation.

10 The immunogenic compositions of the invention can include one or more adjuvants, including, but not limited to aluminum hydroxide; aluminum phosphate; STIMULON™ QS-21 (Aquila Biopharmaceuticals, Inc., Framingham, MA); MPL™ (3-O-deacylated monophosphoryl lipid A; Corixa, Hamilton, MT), 529 (an amino alkyl glucosamine phosphate compound, Corixa, Hamilton, MT), IL-12 (Genetics
15 Institute, Cambridge, MA); GM-CSF (Immunex Corp., Seattle, Washington); N-acetyl-muramyl-L-theronyl-D-isoglutamine (thr-MDP); N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as nor-MDP); N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy-ethylamine) (CGP 19835A, referred to as MTP-PE); and cholera toxin.
20 Others which may be used are non-toxic derivatives of cholera toxin, including its A subunit, and/or conjugates or genetically engineered fusions of the *N. meningitidis* polypeptide with cholera toxin or its B subunit ("CTB"), procholeraenoid, fungal polysaccharides, including schizophyllan, muramyl dipeptide, muramyl dipeptide ("MDP") derivatives, phorbol esters, the heat labile toxin of *E. coli*, block polymers
25 or saponins.

In certain preferred embodiments, the proteins of this invention are used in an immunogenic composition for oral administration which includes a mucosal adjuvant and used for the treatment or prevention of *N. meningitidis* infection in a human host. The mucosal adjuvant can be a cholera toxin; however, preferably, mucosal adjuvants
30 other than cholera toxin which may be used in accordance with the present invention

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include non-toxic derivatives of a cholera holotoxin, wherein the A subunit is mutagenized, chemically modified cholera toxin, or related proteins produced by modification of the cholera toxin amino acid sequence. For a specific cholera toxin which may be particularly useful in preparing immunogenic compositions of this invention, see the mutant cholera holotoxin E29H, as disclosed in Published International Application WO 00/18434, which is hereby incorporated herein by reference in its entirety. These may be added to, or conjugated with, the polypeptides of this invention. The same techniques can be applied to other molecules with mucosal adjuvant or delivery properties such as *Escherichia coli* heat labile toxin (LT). Other compounds with mucosal adjuvant or delivery activity may be used such as bile; polycations such as DEAE-dextran and polyornithine; detergents such as sodium dodecyl benzene sulphate; lipid-conjugated materials; antibiotics such as streptomycin; vitamin A; and other compounds that alter the structural or functional integrity of mucosal surfaces. Other mucosally active compounds include derivatives of microbial structures such as MDP; acridine and cimetidine. STIMULON™ QS-21, MPL, and IL-12, as described above, may also be used.

The immunogenic compositions of this invention may be delivered in the form of ISCOMS (immune stimulating complexes), ISCOMS containing CTB, liposomes or encapsulated in compounds such as acrylates or poly(DL-lactide-co-glycoside) to form microspheres of a size suited to adsorption. The proteins of this invention may also be incorporated into oily emulsions.

Multiple Antigens

The immunogenic agents, including proteins, polynucleotides and equivalents of the present invention may be administered as the sole active immunogen in a immunogenic composition, or alternatively, the composition may include other active immunogens, including other *Neisseria sp.* immunogenic polypeptides, or immunologically-active proteins of one or more other microbial pathogens (e.g. virus, prion, bacterium, or fungus, without limitation) or capsular polysaccharide. The compositions may comprise one or more desired proteins, fragments or pharmaceutical compounds as desired for a chosen indication. In the same manner,

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the compositions of this invention which employ one or more nucleic acids in the immunogenic composition may also include nucleic acids which encode the same diverse group of proteins, as noted above.

Any multi-antigen or multi-valent immunogenic composition is contemplated by the present invention. For example, the compositions of the present invention may 5
comprise combinations of two or more 2086 proteins, a combination of 2086 protein with one or more Por A proteins, a combination of 2086 protein with meningococcus serogroup A, C, Y and W135 polysaccharides and/or polysaccharide conjugates, a combination of 2086 protein with meningococcus and pneumococcus combinations, 10
or a combination of any of the foregoing in a form suitable for mucosal delivery. Persons of skill in the art would be readily able to formulate such multi-antigen or multi-valent immunologic compositions.

The present invention also contemplates multi-immunization regimens wherein any composition useful against a pathogen may be combined therein or 15
therewith the compositions of the present invention. For example, without limitation, a patient may be administered the immunogenic composition of the present invention and another immunological composition for immunizing against *S. Pneumoniae*, as part of a multi-immunization regimen. Persons of skill in the art would be readily able to select immunogenic compositions for use in conjunction with the 20
immunogenic compositions of the present invention for the purposes of developing and implementing multi-immunization regimens.

Specific embodiments of this invention relate to the use of one or more polypeptides of this invention, or nucleic acids encoding such, in a composition or as part of a treatment regimen for the prevention or amelioration of *S. pneumoniae* 25
infection. One can combine the 2086 polypeptides or 2086 polynucleotides with any immunogenic composition for use against *S. pneumoniae* infection. One can also combine the 2086 polypeptides or 2086 polynucleotides with any other protein or polysaccharide-based meningococcal vaccine.

The 2086 polypeptides, fragments and equivalents can be used as part of a conjugate immunogenic composition; wherein one or more proteins or polypeptides are conjugated to a carrier in order to generate a composition that has immunogenic properties against several serotypes and/or against several diseases. Alternatively,
5 one of the 2086 polypeptides can be used as a carrier protein for other immunogenic polypeptides.

The present invention also relates to a method of inducing immune responses in a mammal comprising the step of providing to said mammal an immunogenic composition of this invention. The immunogenic composition is a composition which
10 is antigenic in the treated animal or human such that the immunologically effective amount of the polypeptide(s) contained in such composition brings about the desired immune response against *N. meningitidis* infection. Preferred embodiments relate to a method for the treatment, including amelioration, or prevention of *N. meningitidis* infection in a human comprising administering to a human an immunologically
15 effective amount of the composition.

The phrase “immunologically effective amount,” as used herein, refers to the administration of that amount to a mammalian host (preferably human), either in a single dose or as part of a series of doses, sufficient to at least cause the immune system of the individual treated to generate a response that reduces the clinical impact
20 of the bacterial infection. This may range from a minimal decrease in bacterial burden to prevention of the infection. Ideally, the treated individual will not exhibit the more serious clinical manifestations of the bacterial infection. The dosage amount can vary depending upon specific conditions of the individual. This amount can be determined in routine trials or otherwise by means known to those skilled in the art.

25 Another specific aspect of the present invention relates to using as the immunogenic composition a vector or plasmid which expresses an protein of this invention, or an immunogenic portion thereof. Accordingly, a further aspect this invention provides a method of inducing an immune response in a mammal, which comprises providing to a mammal a vector or plasmid expressing at least one isolated
30 2086 polypeptide. The protein of the present invention can be delivered to the

mammal using a live vector, in particular using live recombinant bacteria, viruses or other live agents, containing the genetic material necessary for the expression of the polypeptide or immunogenic portion as a foreign polypeptide.

According to a further implementation of the present invention, a method is provided for diagnosing bacterial meningitis in a mammal comprising: detecting the presence of immune complexes in the mammal or a tissue sample from said mammal, said mammal or tissue sample being contacted with an antibody composition comprising antibodies that immunospecifically bind with at least one polypeptide comprising the amino acid sequence of any of the even numbered SEQ ID NOS: 2-252; wherein the mammal or tissue sample is contacted with the antibody composition under conditions suitable for the formation of the immune complexes.

Viral and Non-Viral Vectors

Preferred vectors, particularly for cellular assays *in vitro* and *in vivo*, are viral vectors, such as lentiviruses, retroviruses, herpes viruses, adenoviruses, adeno-associated viruses, vaccinia virus, baculovirus, and other recombinant viruses with desirable cellular tropism. Thus, a nucleic acid encoding a 2086 protein or immunogenic fragment thereof can be introduced *in vivo*, *ex vivo*, or *in vitro* using a viral vector or through direct introduction of DNA. Expression in targeted tissues can be effected by targeting the transgenic vector to specific cells, such as with a viral vector or a receptor ligand, or by using a tissue-specific promoter, or both. Targeted gene delivery is described in PCT Publication No. WO 95/28494, which is incorporated herein by reference in its entirety.

Viral vectors commonly used for *in vivo* or *ex vivo* targeting and therapy procedures are DNA-based vectors and retroviral vectors. Methods for constructing and using viral vectors are known in the art (*e.g.*, Miller and Rosman, *BioTechniques*, 1992, 7:980-990). Preferably, the viral vectors are replication-defective, that is, they are unable to replicate autonomously in the target cell. Preferably, the replication defective virus is a minimal virus, *i.e.*, it retains only the sequences of its genome which are necessary for encapsulating the genome to produce viral particles.

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DNA viral vectors include an attenuated or defective DNA virus, such as but not limited to herpes simplex virus (HSV), papillomavirus, Epstein Barr virus (EBV), adenovirus, adeno-associated virus (AAV), and the like. Defective viruses, which entirely or almost entirely lack viral genes, are preferred. Defective virus is not infective after introduction into a cell. Use of defective viral vectors allows for administration to cells in a specific, localized area, without concern that the vector can infect other cells. Thus, a specific tissue can be specifically targeted. Examples of particular vectors include, but are not limited to, a defective herpes virus 1 (HSV1) vector (Kaplitt *et al.*, *Molec. Cell. Neurosci.*, 1991, 2:320-330), defective herpes virus vector lacking a glyco-protein L gene, or other defective herpes virus vectors (PCT Publication Nos. WO 94/21807 and WO 92/05263); an attenuated adenovirus vector, such as the vector described by Stratford-Perricaudet *et al.* (*J. Clin. Invest.*, 1992, 90:626-630; see also La Salle *et al.*, *Science*, 1993, 259:988-990); and a defective adeno-associated virus vector (Samulski *et al.*, *J. Virol.*, 1987, 61:3096-3101; Samulski *et al.*, *J. Virol.*, 1989, 63:3822-3828; Lebkowski *et al.*, *Mol. Cell. Biol.*, 1988, 8:3988-3996), each of which is incorporated by reference herein in its entirety.

Various companies produce viral vectors commercially, including, but not limited to, Avigen, Inc. (Alameda, CA; AAV vectors), Cell Genesys (Foster City, CA; retroviral, adenoviral, AAV vectors, and lentiviral vectors), Clontech (retroviral and baculoviral vectors), Genovo, Inc. (Sharon Hill, PA; adenoviral and AAV vectors), Genvec (adenoviral vectors), IntroGene (Leiden, Netherlands; adenoviral vectors), Molecular Medicine (retroviral, adenoviral, AAV, and herpes viral vectors), Norgen (adenoviral vectors), Oxford BioMedica (Oxford, United Kingdom; lentiviral vectors), and Transgene (Strasbourg, France; adenoviral, vaccinia, retroviral, and lentiviral vectors), incorporated by reference herein in its entirety.

Adenovirus vectors. Adenoviruses are eukaryotic DNA viruses that can be modified to efficiently deliver a nucleic acid of this invention to a variety of cell types. Various serotypes of adenovirus exist. Of these serotypes, preference is given, within the scope of the present invention, to using type 2 or type 5 human adenoviruses (Ad 2 or Ad 5) or adenoviruses of animal origin (*see* PCT Publication

No. WO 94/26914). Those adenoviruses of animal origin which can be used within the scope of the present invention include adenoviruses of canine, bovine, murine (example: Mav1, Beard *et al.*, Virology, 1990, 75-81), ovine, porcine, avian, and simian (example: SAV) origin. Preferably, the adenovirus of animal origin is a canine
5 adenovirus, more preferably a CAV2 adenovirus (*e.g.*, Manhattan or A26/61 strain, ATCC VR-800, for example). Various replication defective adenovirus and minimum adenovirus vectors have been described (PCT Publication Nos. WO 94/26914, WO 95/02697, WO 94/28938, WO 94/28152, WO 94/12649, WO 95/02697, WO 96/22378). The replication defective recombinant adenoviruses according to the
10 invention can be prepared by any technique known to the person skilled in the art (Levrero *et al.*, *Gene*, 1991, 101:195; European Publication No. EP 185 573; Graham, EMBO J., 1984, 3:2917; Graham *et al.*, *J. Gen. Virol.*, 1977, 36:59). Recombinant adenoviruses are recovered and purified using standard molecular biological techniques, which are well known to persons of ordinary skill in the art.

15 **Adeno-associated viruses.** The adeno-associated viruses (AAV) are DNA viruses of relatively small size that can integrate, in a stable and site-specific manner, into the genome of the cells which they infect. They are able to infect a wide spectrum of cells without inducing any effects on cellular growth, morphology or differentiation, and they do not appear to be involved in human pathologies. The
20 AAV genome has been cloned, sequenced and characterized. The use of vectors derived from the AAVs for transferring genes *in vitro* and *in vivo* has been described (*see*, PCT Publication Nos. WO 91/18088 and WO 93/09239; U.S. Patent Nos. 4,797,368 and 5,139,941; European Publication No. EP 488 528). The replication defective recombinant AAVs according to the invention can be prepared by
25 cotransfecting a plasmid containing the nucleic acid sequence of interest flanked by two AAV inverted terminal repeat (ITR) regions, and a plasmid carrying the AAV encapsidation genes (rep and cap genes), into a cell line which is infected with a human helper virus (for example an adenovirus). The AAV recombinants which are produced are then purified by standard techniques.

Retrovirus vectors. In another implementation of the present invention, the nucleic acid can be introduced in a retroviral vector, *e.g.*, as described in U.S. Patent No. 5,399,346; Mann *et al.*, *Cell*, 1983, 33:153; U.S. Patent Nos. 4,650,764 and 4,980,289; Markowitz *et al.*, *J. Virol.*, 1988, 62:1120; U.S. Patent No. 5,124,263; 5 European Publication Nos. EP 453 242 and EP178 220; Bernstein *et al.*, *Genet. Eng.*, 1985, 7:235; McCormick, *BioTechnology*, 1985, 3:689; PCT Publication No. WO 95/07358; and Kuo *et al.*, *Blood*, 1993, 82:845, each of which is incorporated by reference in its entirety. The retroviruses are integrating viruses that infect dividing cells. The retrovirus genome includes two LTRs, an encapsidation sequence and three 10 coding regions (*gag*, *pol* and *env*). In recombinant retroviral vectors, the *gag*, *pol* and *env* genes are generally deleted, in whole or in part, and replaced with a heterologous nucleic acid sequence of interest. These vectors can be constructed from different types of retrovirus, such as, HIV, MoMuLV ("murine Moloney leukaemia virus" MSV ("murine Moloney sarcoma virus"), HaSV ("Harvey sarcoma virus"); SNV 15 ("spleen necrosis virus"); RSV ("Rous sarcoma virus") and Friend virus. Suitable packaging cell lines have been described in the prior art, in particular the cell line PA317 (U.S. Patent No. 4,861,719); the PsiCRIP cell line (PCT Publication No. WO 90/02806) and the GP+envAm-12 cell line (PCT Publication No. WO 89/07150). In addition, the recombinant retroviral vectors can contain modifications within the 20 LTRs for suppressing transcriptional activity as well as extensive encapsidation sequences which may include a part of the *gag* gene (Bender *et al.*, *J. Virol.*, 1987, 61:1639). Recombinant retroviral vectors are purified by standard techniques known to those having ordinary skill in the art.

Retroviral vectors can be constructed to function as infectious particles or to 25 undergo a single round of transfection. In the former case, the virus is modified to retain all of its genes except for those responsible for oncogenic transformation properties, and to express the heterologous gene. Non-infectious viral vectors are manipulated to destroy the viral packaging signal, but retain the structural genes required to package the co-introduced virus engineered to contain the heterologous 30 gene and the packaging signals. Thus, the viral particles that are produced are not capable of producing additional virus.

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Retrovirus vectors can also be introduced by DNA viruses, which permits one cycle of retroviral replication and amplifies transfection efficiency (*see* PCT Publication Nos. WO 95/22617, WO 95/26411, WO 96/39036 and WO 97/19182).

Lentivirus vectors. In another implementation of the present invention,
5 lentiviral vectors can be used as agents for the direct delivery and sustained expression of a transgene in several tissue types, including brain, retina, muscle, liver and blood. The vectors can efficiently transduce dividing and nondividing cells in these tissues, and effect long-term expression of the gene of interest. For a review, *see*, Naldini, Curr. Opin. Biotechnol., 1998, 9:457-63; *see also* Zufferey, *et al.*, *J.*
10 *Virol.*, 1998, 72:9873-80). Lentiviral packaging cell lines are available and known generally in the art. They facilitate the production of high-titer lentivirus vectors for gene therapy. An example is a tetracycline-inducible VSV-G pseudotyped lentivirus packaging cell line that can generate virus particles at titers greater than 10⁶ IU/mL for at least 3 to 4 days (Kafri, *et al.*, *J. Virol.*, 1999, 73: 576-584). The vector
15 produced by the inducible cell line can be concentrated as needed for efficiently transducing non-dividing cells *in vitro* and *in vivo*.

Non-viral vectors. In another implementation of the present invention, the vector can be introduced *in vivo* by lipofection, as naked DNA, or with other transfection facilitating agents (peptides, polymers, etc.). Synthetic cationic lipids can
20 be used to prepare liposomes for *in vivo* transfection of a gene encoding a marker (Felgner, *et. al.*, Proc. Natl. Acad. Sci. U.S.A., 1987, 84:7413-7417; Felgner and Ringold, Science, 1989, 337:387-388; *see* Mackey, *et al.*, *Proc. Natl. Acad. Sci. U.S.A.*, 1988, 85:8027-8031; Ulmer *et al.*, *Science*, 1993, 259:1745-1748). Useful lipid compounds and compositions for transfer of nucleic acids are described in PCT
25 Patent Publication Nos. WO 95/18863 and WO 96/17823, and in U.S. Patent No. 5,459,127. Lipids may be chemically coupled to other molecules for the purpose of targeting (*see* Mackey, *et. al.*, *supra*). Targeted peptides, *e.g.*, hormones or neurotransmitters, and proteins such as antibodies, or non-peptide molecules could be coupled to liposomes chemically.

Other molecules are also useful for facilitating transfection of a nucleic acid *in vivo*, such as a cationic oligopeptide (*e.g.*, PCT Patent Publication No. WO 95/21931), peptides derived from DNA binding proteins (*e.g.*, PCT Patent Publication No. WO 96/25508), or a cationic polymer (*e.g.*, PCT Patent Publication No.

5 WO 95/21931).

It is also possible to introduce the vector *in vivo* as a naked DNA plasmid. Naked DNA vectors for vaccine purposes or gene therapy can be introduced into the desired host cells by methods known in the art, *e.g.*, electroporation, microinjection, cell fusion, DEAE dextran, calcium phosphate precipitation, use of a gene gun, or use
10 of a DNA vector transporter (*e.g.*, Wu *et al.*, *J. Biol. Chem.*, 1992, 267:963-967; Wu and Wu, *J. Biol. Chem.*, 1988, 263:14621-14624; Canadian Patent Application No. 2,012,311; Williams *et al.*, *Proc. Natl. Acad. Sci. USA*, 1991, 88:2726-2730). Receptor-mediated DNA delivery approaches can also be used (Curiel *et al.*, *Hum. Gene Ther.*, 1992, 3:147-154; Wu and Wu, *J. Biol. Chem.*, 1987, 262:4429-4432).

15 U.S. Patent Nos. 5,580,859 and 5,589,466 disclose delivery of exogenous DNA sequences, free of transfection facilitating agents, in a mammal. Recently, a relatively low voltage, high efficiency *in vivo* DNA transfer technique, termed electrotransfer, has been described (Mir *et al.*, *C.P. Acad. Sci.*, 1988, 321:893; PCT Publication Nos. WO 99/01157; WO 99/01158; WO 99/01175). Accordingly, additional embodiments

20 of the present invention relates to a method of inducing an immune response in a human comprising administering to said human an amount of a DNA molecule encoding a 2086 polypeptide of this invention, optionally with a transfection-facilitating agent, where said polypeptide, when expressed, retains immunogenicity and, when incorporated into an immunogenic composition and administered to a
25 human, provides protection without inducing enhanced disease upon subsequent infection of the human with *Neisseria sp.* pathogen, such as *N. meningitidis*.

Transfection-facilitating agents are known in the art and include bupivacaine, and other local anesthetics (for examples see U.S. Patent No. 5,739,118) and cationic polyamines (as published in International Patent Application WO 96/10038), which
30 are hereby incorporated by reference.

The present invention also relates to an antibody, which may either be a monoclonal or polyclonal antibody, specific for 2086 polypeptides as described above. Such antibodies may be produced by methods which are well known to those skilled in the art.

5 **Bacterial Expression Systems and Plasmids**

This invention also provides a recombinant DNA molecule, such as a vector or plasmid, comprising an expression control sequence having promoter sequences and initiator sequences and a nucleotide sequence which codes for a polypeptide of this invention, the nucleotide sequence being located 3' to the promoter and initiator
10 sequences. In yet another aspect, the invention provides a recombinant DNA cloning vehicle capable of expressing a 2086 polypeptide comprising an expression control sequence having promoter sequences and initiator sequences, and a nucleotide sequence which codes for a 2086 polypeptide, the nucleotide sequence being located 3' to the promoter and initiator sequences. In a further aspect, there is provided a host
15 cell containing a recombinant DNA cloning vehicle and/or a recombinant DNA molecule as described above. Suitable expression control sequences and host cell/cloning vehicle combinations are well known in the art, and are described by way of example, in Sambrook *et al.* (1989).

Once recombinant DNA cloning vehicles and/or host cells expressing a
20 desired *a* polypeptide of this invention have been constructed by transforming, transfecting or infecting such cloning vehicles or host cells with plasmids containing the corresponding 2086 polynucleotide, cloning vehicles or host cells are cultured under conditions such that the polypeptides are expressed. The polypeptide is then isolated substantially free of contaminating host cell components by techniques well
25 known to those skilled in the art.

The following examples are included to demonstrate preferred embodiments of the invention. It should be appreciated by those skilled in the art that the techniques disclosed in the examples which follow represent techniques discovered by the inventors to function well in the practice of the invention, and thus can be

considered to constitute preferred modes for its practice. However, those of skill in the art should, in view of the present disclosure, appreciate that many changes can be made in the specific embodiments which are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

5

EXAMPLES

Example 1

Identification of a neisserial membrane protein extract capable of eliciting bactericidal antibodies against heterologous strains:

Referring to Table II below, LOS-depleted outer membrane protein preparations have been shown to elicit bactericidal antibodies. These antibodies are often directed towards the PorA of the respective strain. LOS-depleted outer membrane preparations from serogroup B meningococcal strain 8529 (B:15:P1.7b,3) are unusual in this manner because they unexpectedly elicit bactericidal antibodies to several heterologous strains.

TABLE II

BC Activity of Anti-sOMPS Against Different Strains of *N. meningitidis*

Anti-serum Week 6	H44/76	5315	H355	M982	880049	8529*	NMB
Serosubtype	P1.7,16	P1.5	P1.15	P1.9	P1.4	P1.3	P1.5,2
sOMPs H44/76 25µg QS-21 20µg	1,000	< 50	< 50	< 50	< 50	980	< 50
sOMPs 5315 25µg QS-21 20µg	50	< 50	<50	< 50	< 50	2170	< 50
sOMPs H355 25µg QS-21 20µg	< 50	< 50	450	< 50	< 50	860	< 50
sOMPs M982 25µg QS-21 20µg	92	< 50	< 50	300	< 50	1100	< 50
sOMPs 880049 25µg QS-21 20µg	50	< 50	< 50	< 50	< 50	1190	< 50
sOMPs 8529 25µg QS-21 20µg	1,000	< 50	450	50	215	>4050 (81.7)	< 50
sOMPs 2996 25µg QS-21 20µg	< 50	< 50	< 50	< 50	< 50	790	148

Whole-cell control serum 25µg 3DMPL 25µg	450	50	100	500	150	>1350 (66.0)	952
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To facilitate the isolation and characterization of the antigen(s) responsible for eliciting heterologous bactericidal antibodies, we sought to identify which detergent optimally extracted the antigen(s)

5 Strains and culture conditions.

N. meningitidis strain 8529 from a frozen vial was streaked onto a GC plate. (The meningococcal strain 8529 was received from The RIVM, Bilthoven, The Netherlands). The plate was incubated at 36°C/5%CO₂ for 7.5h. Several colonies were used to inoculate a flask containing 50 mL of modified Frantz medium + GC supplement. The flask was incubated in an air shaker at 36°C and agitated at 200 RPM for 4.5h. 5 mL was used to inoculate a Fernbach flask containing 450 mL of modified Frantz medium + GC supplement. The flask was incubated in an air shaker at 36°C and agitated at 100 RPM for 11h. The entire 450 mL was used to inoculate 8.5 L of modified Frantz medium+ GC supplement in a 10 L fermentor.

15

Composition of Modified Frantz Medium:

	Glutamic acid	1.3 g/L
	Cysteine	0.02
20	Sodium phosphate, dibasic, 7 hydrate	10
	Potassium chloride	0.09
	Sodium chloride	6
	Ammonium chloride	1.25
	Dialyzed yeast extract (YE)	40 ml
25	(25% YE soln. dialyzed against 5 volumes of dH ₂ O overnight, then autoclaved)	

GC supplement 100X, filter sterilize

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	Dextrose	400 g/L
	Glutamic acid	10
	Coccarboxylase	0.02
5	Ferric nitrate	0.5

The following parameters were controlled during fermentation:

Temperature=36°C ; pH=7.4; Dissolved Oxygen=20%. Several drops of P-2000 antifoam were added to control foaming. The culture was grown to stationary phase.

- 10 Cells were harvested by centrifugation at OD650=5.25. A total of 100-300 grams of wet cell paste is typically harvested from ~8.5L of culture.

Partial purification of outer membrane protein fractions from meningococci which elicit heterologous bactericidal antibodies:

- 100 gms wet weight of cells were suspended, to a volume five times the wet weight, with 10mM HEPES-NaOH, pH 7.4, 1mM Na₂EDTA and lysed by passage through a 110Y microfluidizer equipped with a chamber at ~18,000 psi. The cell lysate was clarified and the cell envelope isolated by centrifugation at 300,000 x g for 1 hour at 10°C. The cell envelopes were washed 2X with the same buffer by suspension with a homogenizer followed by centrifugation as above. The cell envelopes were then extracted with 320mL of 1% (w/v) Triton X-100 in 10mM HEPES-NaOH, pH 7.4, 1mM MgCl₂. Referring to Table III below, results from sequential differential detergent extraction using Triton X-100 and Zwittergent 3-14 followed by immunization of mice, allowed us to determine that the Triton extracts optimally extracted the candidate(s) of interest. This Triton X-100 extract, eliciting bactericidal antibody response against 4 out of five strains listed in table III, was then fractionated by preparative isoelectric focusing (IEF) in a BioRad Rotaphor unit. Ampholyte concentrations were 1% pH 3-10 mixed with 1% pH 4-6. As shown in Table III, several fractions were found to elicit a heterologous bactericidal response. The fractions obtained from IEF, which focused in the pH range of 5.5-7.8, elicited a

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heterologous response to the most strains as determined by the bactericidal assay.

The pooled IEF fractions were concentrated and the ampholytes removed by ethanol precipitation. A further purification was achieved by adsorbing some of the proteins obtained in the pH range of about 5.5-7.8 on an anion exchange column and

- 5 comparing the bactericidal activity obtained after immunizing mice with the adsorbed and unadsorbed proteins. Referring again to Table II, while many proteins were adsorbed to the anion exchange resin, the proteins which were not adsorbed by the column elicited more heterologous bactericidal antibodies.

TABLE III

Method	Fraction	BC ₅₀ Target Strain				
		H44/76	880049	H355	539*	M982
LOS-depleted	sOMPs	1,000	215	450	NC	50
Detergent Extractions	<u>Cytoplasmic Extract</u>	200	NT	NT	NT	NT
	TX-100	>800	>800	>800	>800	<25
	Zwittergent 3-12	400	>25	100	400	<25
	Zwittergent 3-14	<25	NT	NT	NT	NT
	Zw.3-14 + NaCl	<25	NT	NT	NT	NT
	Sarcosyl	<25	NT	NT	NT	NT
	Zw.3-14 + heat	<25	NT	NT	NT	NT
Preparative IEF	Fractions 1-3 (pH 2.3-3.9)	50	NT	NT	NT	NT
	Fraction 4 (pH 4.1)	>800	<25	100	<25	NT
	Fraction 5 (pH 4.3)	>800	<25	100	200	NT
	Fraction 6 (pH 4.5)	400	NT	NT	NT	NT
	Fraction 7 (pH 4.8)	<25	NT	NT	NT	NT
	Fractions 8-9 (pH 5.0-5.3)	<25	NT	NT	NT	NT
	Fractions 10-17 (pH 5.5-7.8)	>800	200	<800	<800	NT
Anion Exchange	Adsorbed	400	NT	100	100	NT
	Unadsorbed	>6,400	NT	<800	<800	NT

10 NT: not tested

*Clinical isolate 539 is a homologous strain to 8529, isolated from the same outbreak

- As shown in FIG. 1A, two major proteins were present in the unadsorbed fraction as determined by SDS-PAGE. To identify these proteins, two types of analysis were performed. One analysis was to perform limited proteolytic degradation (See FIG. 1A, and FIG. 1B) followed by isolation of peptides and direct protein sequencing. The other analysis was to perform SDS-PAGE followed by gel
- 15

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excision, proteolytic digestion, and LC-MS/MS (Liquid Chromotography tandem Mass Spectrometry), (see FIG. 3) to obtain mass spectral information on the components of the preparations of interest. (See peptide mapping and sequencing methods described later in this section)

5 The *N. meningitidis* A Sanger genomic sequence was analyzed using the methods and algorithms described in Zagursky and Russell, 2001, *BioTechniques*, 31:636-659. This mining analysis yielded over 12,000 possible Open Reading Frames (ORFs). Both the direct sequence data and the mass spectral data described above indicated that the major components of the unadsorbed fraction were the
10 products of several ORFs present in an analysis of the Sanger database. The three predominant proteins identified by this methodology correspond to ORFs 4431, 5163 and 2086, (see FIGS. 1B and 3).

 Although ORF 4431 was the most predominant protein identified in the fractions, mouse antibodies to recombinant lipidated 4431 were not bactericidal and
15 did not provide a protective response in an animal model. Additional analysis of ORF 5163 is in progress.

 The second most predominant component of the preparations described herein corresponds to the product of ORF 2086.

Immunogenicity Methods:

20 Preparation of antisera:

 Except where noted, protein compositions/vaccines were formulated with 25µg of total protein and were adjuvanted with 20µg QS-21. A 0.2mL dose was administered by subcutaneous (rump) injection to 6-8 week old female Swiss-Webster mice at week 0 and 4. Bleeds were collected at week 0 and 4, and a final
25 exsanguination bleed was performed on week 6.

Bactericidal assay:

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Bactericidal assays were performed essentially as described (See Mountzouros and Howell, 2000, *J. Clin. Microbiol.* 38(8):2878-2884). Complement-mediated antibody-dependent bactericidal titers for the SBA were expressed as the reciprocal of the highest dilution of test serum that killed $\geq 50\%$ of the target cells introduced into the assays (BC₅₀ titer).

Methods used to identify 2086 protein:

Cyanogen Bromide cleavage and direct sequencing of fragments:

Cyanogen Bromide cleavage of Anion Exchange Unadsorbed Fraction (AEUF). The AEUF was precipitated with 90% cold ethanol and was solubilized with 10mg/mL cyanogen bromide in 70% formic acid to a protein concentration of 1mg/mL. The reaction was performed overnight at room temperature in the dark. The cleaved products were dried down by speed vacuum, and the pellet was solubilized with HE/0.1% reduced TX-100. SDS-PAGE followed by N-terminal amino acid sequencing were used to identify the components of this fraction.

Protease digestion/reverse phase/N-terminal sequencing to identify components:

The AEUF was digested with either GluC (V8), LysC or ArgC. The protein to enzyme ratio was 30 μ g protein to 1 μ g enzyme. The digestion was carried out at 37°C overnight. The digested protein mixture (30 μ g) was passed over a seven micron Aquapore RF-300 column and was eluted with a gradient of 10-95% acetonitrile in 0.1% trifluoroacetic acid, and peaks were collected manually. A no protein blank was also run, and the peaks from this were subtracted from the sample chromatogram. Peaks occurring only in the sample run were analyzed by mass spectrometer, and those samples giving a clear mass were analyzed for N-terminal amino acid sequencing.

N-terminal amino acid sequencing:

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For bands excised from a blot, the protein sample is transferred from an SDS gel to a PVDF membrane, stained with Amido Black (10% acetic acid, 0.1% amido black in deionized water) and destained in 10% acetic acid. The desired protein band is then excised from all ten lanes using a methanol cleaned scalpel or mini-Exacto
5 knife and placed in the reaction cartridge of the Applied Biosystems 477A Protein Sequencer. For direct sequencing of samples in solution, the Prosorb cartridge is assembled and the PVDF wetted with 60 μ L of methanol. The PVDF is rinsed with 50 μ L of deionized water and the sample (50 μ L) is loaded to the PVDF. After 50 μ L of deionized water is used to rinse the sample, the Prosorb PVDF is punched out,
10 dried, and placed in the reaction cartridge of the Applied Biosystems 477A Protein Sequencer. For both methods, the Applied Biosystems N-terminal Sequencer is then run under optimal blot conditions for 12 or more cycles (1 cycle Blank, 1 cycle Standard, and 10 or more cycles for desired residue identification) and PTH-amino acid detection is done on the Applied Biosystems 120A PTH Analyzer. The cycles
15 are collected both on an analog chart recorder and digitally via the instrument software. Amino acid assignment is done using the analog and digital data by comparison of a standard set of PTH-amino acids and their respective retention times on the analyzer (cysteine residues are destroyed during conversion and are not detected). Multiple sequence information can be obtained from a single residue and
20 primary versus secondary assignments are made based on signal intensity.

LC-MS/MS

Protein samples purified by IEF were further analyzed by SDS-polyacrylamide gel electrophoresis. Proteins were visualized by Coomassie blue staining, and bands of interest were excised manually, then reduced, alkylated and
25 digested with trypsin (Promega, Madison, WI) *in situ* using an automated in-gel tryptic digestion robot (1). After digestion, peptide extracts were concentrated to a final volume of 10-20 μ L using a Savant Speed Vac Concentrator (ThermoQuest, Holdbrook, NY).

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Peptide extracts were analyzed on an automated microelectrospray reversed phase HPLC. In brief, the microelectrospray interface consisted of a Picofrit fused silica spray needle, 50 cm length by 75 μ m ID, 8 μ m orifice diameter (New Objective, Cambridge MA) packed with 10 μ m C18 reversed-phase beads (YMC, Wilmington, NC) to a length of 10 cm. The Picofrit needle was mounted in a fiber optic holder (Melles Griot, Irvine, CA) held on a home-built base positioned at the front of the mass spectrometer detector. The rear of the column was plumbed through a titanium union to supply an electrical connection for the electrospray interface. The union was connected with a length of fused silica capillary (FSC) tubing to a FAMOS autosampler (LC-Packings, San Francisco, CA) that was connected to an HPLC solvent pump (ABI 140C, Perkin-Elmer, Norwalk, CT). The HPLC solvent pump delivered a flow of 50 μ L/min which was reduced to 250 nL/min using a PEEK microtight splitting tee (Upchurch Scientific, Oak Harbor, WA), and then delivered to the autosampler using an FSC transfer line. The LC pump and autosampler were each controlled using their internal user programs. Samples were inserted into plastic autosampler vials, sealed, and injected using a 5 μ L sample loop.

Microcapillary HPLC-mass spectrometry:

Extracted peptides from in-gel digests were separated by the microelectrospray HPLC system using a 50 minute gradient of 0-50% solvent B (A: 0.1M HoAc, B: 90% MeCN/0.1M HoAc). Peptide analyses were done on a Finnigan LCQ ion trap mass spectrometer (ThermoQuest, San Jose, CA) operating at a spray voltage of 1.5 kV, and using a heated capillary temperature of 150 °C. Data were acquired in automated MS/MS mode using the data acquisition software provided with the instrument. The acquisition method included 1 MS scan (375-1200 m/z) followed by MS/MS scans of the top 3 most abundant ions in the MS scan. The dynamic exclusion and isotope exclusion functions were employed to increase the number of peptide ions that were analyzed (settings: 3 amu = exclusion width, 3 min = exclusion duration, 30 secs = pre-exclusion duration, 3 amu = isotope exclusion width). Automated analysis of MS/MS data was performed using the SEQUEST computer algorithm incorporated into the Finnigan Bioworks data analysis package

(ThermoQuest, San Jose, CA) using the database of proteins derived from the complete genome of *N. meningitidis* (from Sanger). The results of the study are illustrated in FIG. 3.

5 **Example 2**

Cloning of Recombinant Lipidated P2086 (rLP2086):

A.) Native Leader Sequence:

Source materials:

10 The ORF 2086 gene was amplified by PCR from a clinical isolate of a serogroup B *Neisseria meningitidis* strain designated 8529. The serogroup, serotype and serosubtype of this strain is shown in parentheses; 8529 (B:15, P1:7b,3). This meningococcal strain was received from The RIVM, Bilthoven, The Netherlands. The mature 2086 protein gene sequence from meningococcal strain 8529 is provided herein as SEQ ID. NO. 212.

15 **PCR Amplification and Cloning Strategy:**

A visual inspection of ORF 2086 indicated that this gene had a potential lipoprotein signal sequence. Additional analysis using a proprietary Hidden Markov Model Lipoprotein algorithm confirmed that ORF 2086 contains a lipoprotein signal sequence. In order to recombinantly express P2086 in a more native-like
20 conformation, oligonucleotide primers were designed to amplify the full length gene with the lipoprotein signal sequence intact and were based on an analysis of the Sanger sequence for *N. meningitidis* A ORF 2086, (5' primer – CT ATT CTG CAT ATG ACT AGG AGC and 3' primer – GCGC GGATCC TTA CTG CTT GGC GGC AAG ACC), which are SEQ ID NO. 304 (Compound No. 4624) and SEQ ID
25 NO. 303 (Compound No. 4623), respectively (See also Table IV herein). The 2086 gene was amplified by polymerase chain reaction (PCR) [ABI 2400 thermal cycler, Applied Biosystems, Foster City, CA] from *N. meningitidis* strain 8529. The correct

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size amplified product was ligated and cloned into pCR2.1-TOPO (Invitrogen). The plasmid DNA was restriction digested with NdeI and BamHI, gel purified and ligated into pET-27b(+) vector (Novagen).

- Oligonucleotide primers described herein, were synthesized on a PerSeptive Biosystems oligonucleotide synthesizer, Applied Biosystems, Foster City CA, using β -Cyanoethylphosphoramidite chemistry, Applied Biosystems, Foster City CA. The primers used for PCR amplification of the ORF 2086 gene families are listed in Table IV, which shows non-limiting examples of primers of the present invention.

10 **TABLE IV: PRIMERS**

SEQ ID NO. (Compound No.)	Primer	Sequence	Restriction sites
303 (4623)	Reverse	GCGCGGATCCCTTACTGCTTGGCGGCAAGACC	BamHI
304 (4624)	Forward	CTATTCTGCATATGACTAGGAGC	NdeI
305 (4625)	Forward	AGCAGCGGAGGCGGCGGTGTC	
306 (5005)	Forward	TGCCGATGCACTAACCGCACC	
307 (5007)	Reverse	CGTTTCGCAACCATCTTCCCG	
308 (5135)	Reverse	GAGATCTCACTCACTCATTACTGCTTGGC GGCAAGACCGATATG	BglII
309 (5658)	Forward	GCGGATCCAGCGGAGGGGTGGTGTGCGCC	BamHI
310 (5660)	Reverse	GCGCATGCTTACTGCTTGGCGGCAAGACC GATATG	SphI
311 (6385)	Forward	GCGGATCCAGCGGAGGCGGCGGAAGC	BamHI
312 (6406)	Forward	GCGCAGATCTCATATGAGCAGCGGAGGGG GTGGTGTGCGCCCGAYATWGGTGCAGGG CTTGCCG	BglII and NdeI
313 (6470)	Forward	CTATTCTGCGTATGACTAG	
314 (6472)	Reverse	GTCCGAACGGTAAATTATCGTG	
315 (6473)	Forward	GCGGATCCAGCGGAGGCGGCGGTGTGCGCC	BamHI
316 (6474)	Forward	GAGATCTCATATGAGCAGCGGAGGCGGCG GAAGC	BglII and NdeI
317 (6495)	Forward	GACAGCCTGATAAACC	
318	Reverse	GATGCCGATTTCGTGAACC	

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SEQ ID NO. (Compound No.)	Primer	Sequence	Restriction sites
(6496)			
319 (6543)	Reverse	GCGCATGCCTACTGTTTGCCGGCGATG	SphI
320 (6605)	Reverse	GAGATCTCACTCACTCACTACTGTTTGCC GGCGATGCCGATTTC	BglII
321 (6721)	Forward	GCGCAGATCTCATATGAGCAGCGGAGGCG GCGGAAGCGGAGGCGGCGGTGTCACCGCC GACATAGGCACG	BglII and NdeI

rLP2086 lipoprotein expression utilizing native leader sequence:

Referring to FIG. 5, plasmid pPX7340 was transformed/transfected or infected into BLR(DE3) pLysS host cells (Life Sciences). One transformant was selected and inoculated into 50 mL of Terrific Broth containing 2% glucose, kanamycin (30µg/mL), chloramphenicol (30µg/mL), and tetracycline (12µg/mL). The OD600 for the overnight culture was 6.0. The overnight culture was diluted out in 1 liter of Terrific Broth with 1% glycerol and the same antibiotics. The starting OD600 was 0.4. After 2 hours the OD600 was 1.6 and a pre-induced sample was taken. Cells equivalent to an OD600=1 were centrifuged and the supernatant was removed. The whole cell pellet was resuspended in 150µL Tris-EDTA buffer and 150µL of 2x SDS-PAGE sample buffer. IPTG was added to a final concentration of 1mM. After 3.5 hours a post-induced sample was taken as described and analyzed on SDS-PAGE (See FIG. 4).

Purification of rLP2086:

The rLP2086 was solubilized from *E. coli* following differential detergent extraction. Unlike the P2086 in its native environment, the rLP2086 was not significantly solubilized by Triton X-100 or Zwittergent 3-12. The bulk of the rLP2086 was solubilized with sarcosyl, indicating that it interacts with the outer membrane components of *E. coli* differently than it does in *N. meningitidis*. Once solubilized the rLP2086 was purified similarly to the native protein in that many of the contaminating *E. coli* proteins could be removed by adsorption to an anion exchange resin at pH 8. Despite being greater than one half a pH unit above its

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theoretical pI, the rLP2086 remained unadsorbed at pH 8. Further purification was achieved by adsorption of the rLP2086 to a cation exchange resin at pH 4.5.

The homogeneity of the rLP2086 is shown in FIG. 2 following SDS-PAGE. The mass of rLP2086 was determined by MALDI-TOF mass spectral analysis to be 27,836. This mass differs from the theoretical mass of 27,100 by 736, which approximates the mass of the N-terminal lipid modification common to bacterial lipoproteins. Both native and rLP2086 appear to be outer membrane lipoproteins. Attempts with N-terminal sequencing were blocked and this is consistent with the terminal modification.

10

Purification Methods:

Frozen pellets of BLR DE3 pLysS cells expressing P2086 were resuspended in 10mM HEPES-NaOH/1mM EDTA/1μg/mL Pefabloc SC protease inhibitor (Roche) pH 7.4 (HEP) at 20mL/g wet cell weight and lysed by microfluidizer (Microfluidics Corporation Model 110Y). The cell lysate was centrifuged at 150,000 x g for one hour. The pellet was washed twice with HEP and centrifuged twice, and the resulting membrane pellet was frozen overnight. The pellet was solubilized with 10mM HEPES-NaOH/1mM MgCl₂/1%TX-100 pH 7.4 for 30 minutes, followed by centrifugation at 150,000 x g for 30 minutes. This was repeated three times. The membrane pellet was washed as above twice with 50mM Tris-HCl/5mM EDTA/1% Zwittergent 3-12 pH 8, followed by two washes each of 50mM Tris-HCl/5mM EDTA/1% Zwittergent 3-14 pH 8 and 50mM Tris-HCl/5mM EDTA/1% Zwittergent 3-14/ 0.5M NaCl pH 8.

The rLP2086 was then solubilized with 50mM Tris-HCl/5mM EDTA/ 1% sarcosyl pH 8. This sarcosyl extract was adjusted to 1% Zwittergent 3-14 (Z3-14) and dialyzed twice against a 30 fold excess of 50mM Tris-HCl/5mM EDTA/1% Z3-14. The dialyzed rLP2086 extract was precipitated with 90% ethanol to remove remaining sarcosyl, and solubilized with 50mM Tris-HCl/5mM EDTA/ 1% Z3-14 pH 8 (TEZ).

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Insoluble material was removed by centrifugation, the supernatant was passed over an anion exchange chromatography column, and rLP2086 was collected in the unbound fraction. The unbound material was then dialyzed twice against a 30 fold excess of 25mM NaAc/1% Z3-14 pH 4.5, and passed over a cation exchange chromatography column. The rLP2086 was eluted with a 0-0.3M NaCl gradient and analyzed by SDS-PAGE (Coomassie stain). The rLP2086 pool was determined to be 84% pure by laser densitometry.

Surface Reactivity and Bactericidal Activity of Antisera to rLP2086 Subfamily B.

Referring to Table VII, antisera to purified rLP2086 from the Subfamily B strain 8529, demonstrated surface reactivity to all ten 2086 Subfamily B strains tested by whole cell ELISA. Bactericidal activity was detected against nine of ten 2086 Subfamily B strains expressing heterologous serosubtype antigens, PorAs. These strains are representative of strains causing serogroup B meningococcal disease throughout western Europe, the Americas, Australia, and New Zealand. The only strain which was not killed in the bactericidal assay, 870227, reacted strongly with the anti-rLP2086 (Subfamily B) sera by whole cell ELISA, indicating that this strain expresses a protein with epitopes in common to P2086.

The 2086 Subfamily A strains listed in Table VII, were also tested for surface reactivity by whole cell ELISA. Two out of three of these strains appeared to have a very low level of reactivity, indicating that some 2086 Subfamily A strains may not be cross-reactive with antibodies raised to rLP2086 Subfamily B. The PCR amplification procedure used to identify the 2086 Subfamily B gene from strain 8529 was also performed on strains 870446, NMB and 6557. No 2086 Subfamily B PCR amplified product was detected.

Immunogenicity Methods :

Preparation of antisera:

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Vaccines were formulated as described previously in Example 1. However, a 10 µg dose was used.

Whole cell enzyme-linked immunosorbant assay (ELISA):

N. meningitidis whole cell suspensions were diluted to an optical density of 0.1 at 620nm in sterile 0.01M phosphate, 0.137M NaCl, 0.002M KCl (PBS). From this suspension, 0.1mL were added to each well of Nunc Bac T 96 well plates (Cat# 2-69620). Cells were dried on the plates at room temperature for three days, then were covered, inverted and stored at 4°C. Plates were washed three times with wash buffer (0.01M Tris-HCl, 0.139M NaCl/KCl, 0.1% dodecylpoly(oxyethylereneglycolether)_n n=23 (Brij-35®, available from ICI Americas, Inc., Wilmington, Delaware), pH 7.0-7.4). Dilutions of antisera were prepared in PBS, 0.05% Tween-20/Azide and 0.1mL was transferred to the coated plates. Plates were incubated for two hours at 37°C. Plates were washed three times in wash buffer. Goat-anti-mouse IgG AP (Southern Biotech) was diluted at 1:1500 in PBS/0.05% Tween-20, 0.1mL was added to each well, and plates were incubated at 37°C for two hours. Plates were washed (as above). Substrate solution was prepared by diluting p-nitrophenyl phosphate (Sigma) in 1M diethanolamine/0.5mM MgCl₂ to 1mg/mL. Substrate was added to the plate at 0.1mL per well and incubated at room temperature for one hour. The reaction was stopped with 50µL /well of 3N NaOH and plates were read at 405nm with 690nm reference.

B.) P4 Leader Sequence:**PCR Amplification and Cloning Strategy:**

In order to optimize rLP2086 expression, the 2086 gene was cloned behind the P4 signal sequence of nontypable *Haemophilus influenzae* (Green *et al.*, 1991). Primers utilized for lipoprotein cloning are listed in Table IV and are identified by compound numbers: 5658, 5660, 6473, 6543 and 6385. ORF 2086 was amplified from *N. meningitidis* B strain 8529 using primers with the following compound

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numbers 5658 and 5660. ORF 2086 was amplified from *N. meningitidis* serogroup B strain CDC1573 using primers with the following compound numbers 6385 and 5660. ORF 2086 was amplified from *N. meningitidis* serogroup B strain 2996 using primers with the following compound numbers 6473 and 6543. The N-terminal (5') primers
5 were designed to be homologous to the mature region of the 2086 gene (starting at the serine residue at amino acid position 3 just downstream of the cysteine). The restriction site BamHI (GGATTC) was incorporated into the 5' end of each N-terminal primer and resulted in the insertion of a glycine residue in the mature protein at amino acid position 2. The C-terminal (3') primers were designed to be
10 homologous to the C-terminal end of the 2086 gene and included the Stop codon as well as an SphI site for cloning purposes. The amplified fragment from each *N. meningitidis* B strain was cloned into an intermediate vector and screened by sequence analysis.

Plasmid DNA from correct clones was digested with BamHI and SphI
15 restriction enzymes (New England Biolabs, (NEB)). A vector designated pLP339 (supplied by applicants' assignee) was chosen as the expression vector. This vector utilizes the pBAD18-Cm backbone (Beckwith *et al.*, 1995) and contains the P4 lipoprotein signal sequence and P4 gene of nontypable *Haemophilus influenzae* (Green *et al.*, 1991). The pLP339 vector was partially digested with the restriction
20 enzyme BamHI and then subjected to SphI digestion. The amplified 2086 fragments (BamHI/SphI) were each ligated separately into the pLP339 vector (partial BamHI/SphI). This cloning strategy places the mature 2086 gene behind the P4 lipoprotein signal sequence. The BamHI site remains in the cloning junction between the P4 signal sequence and the 2086 gene (See the plasmid construct shown in FIG.
25 7). The following is an example of the sequence at the BamHI cloning junction:

[P4 signal sequence]– TGT GGA TCC –[remaining 2086 mature nucleic acid sequence]

[P4 signal sequence]– Cys Gly Ser –[remaining 2086 mature amino acid sequence]

Referring to FIG. 7, each amplified fragment was cloned into a modified pBAD18-Cm vector containing the P4 leader sequence. Fermentation was performed on recombinant *E. coli* BLR pPX7343 which expresses rP4LP2086 (recombinant P4
5 lipidated 2086) to try to increase the cell density by adding additional glucose. The fermentor was filled with 10L complete M9 Minimal medium, according to Sambrook, supplemented with 1% glucose.

The initial concentration of glucose in the fermentor was 45g/L. The fermentor was inoculated to initial OD of ~0.25. At ~OD 25, additional 20g/L glucose
10 was added. The culture was induced with 1% arabinose at glucose depletion at OD 63.4. The fermentation continued until 3 hours after induction. Samples were saved at t=0, 1, 2, 3 post induction and protein quantified using BSA. At t=3, protein yield is ~0.35 g/L, and 7% total cellular protein. A total of 895 grams of wet cell paste was harvested from ~10 L of culture.

15 Purification of the rP4LP2086 was performed using the same methods as described above in Example 2, section A.

Example 3

Development Genetics for Non-lipidated Mature 2086 Protein:

20 To further evaluate the immunogenicity of the 2086 protein, cloning and expression of the non-lipidated form of P2086 were performed.

PCR gene amplification of the ORF 2086:

Oligonucleotides used for PCR amplification of the non-lipidated 2086 gene are listed in the primer table, Table IV. The 2086 gene from strain 8529 can be amplified with primers
25 identified by compound numbers 5135 and 6406 (SEQ ID NOS. 308 and 312, respectively), as indicated in the table. The 2086 gene from strain CDC1573 can be amplified with primers

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identified by compound numbers 5135 and 6474 (SEQ ID NOS. 308 and 316, respectively). The 2086 gene from strain 2996 can be amplified with primers identified by compound numbers 6406 and 6605 (SEQ ID NOS. 312 and 320, respectively).

5 Features of these primers include, a synthetic BglII restriction site in each primer, a synthetic NdeI restriction site in compound numbers 6406 and 6474 and termination codons in all three reading frames are present in compound numbers 5135 and 6605. Primer numbers 6406 and 6474 amplify the 2086 gene with an ATG (Met) fused to the second amino terminal codon (ACG) representing a single amino acid
10 substitution (replaces TGC Cys) of the mature 2086 polypeptide.

The PCR cloning vector was TOPO-PCR2.1, Invitrogen, Valencia, CA.

The vector used to express non-lipidated 2086 protein was pET9a from Novagen,
15 Madison, WI.

The *E.coli* cloning strain was Top10, Invitrogen, Carlsbad, CA.

The *E. coli* expression strain was BLR(DE3)pLysS, Novagen, Madison, WI.
20

The culture media for cloning purposes was Terrific Broth liquid or agar, according to Sambrook *et al.*, with 1% sterile glucose substituted for glycerol, and the appropriate antibiotic (ampicillin or kanamycin).

25 Plasmid purification was with Qiagen Spin Miniprep Kit (Valencia, CA).

Preparation of the production strain or cell line for Non-lipidated 2086 expression:

The 2086 gene was amplified by polymerase chain reaction (PCR) [AmpliTaq and ABI 2400 thermal cycler, Applied Biosystems, Foster City, CA] from chromosomal DNA
30 derived from meningococcal strain 8529. The PCR amplification of the 2086 gene utilized two oligonucleotide primers in each reaction identified by compound numbers 6474 and 5135 (SEQ ID NOS. 316 and 308, respectively). The amplified 2086 PCR product was cloned

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directly into the TOPO-PCR2.1 cloning vector and selected on Terrific Broth agar supplemented with 100 µg/ml ampicillin and 20 µg/ml X-Gal. White colonies were selected and grown. Plasmid DNA was prepared using a Qiagen miniprep kit and the plasmids were screened for the PCR fragment insert. PCR insert plasmids were subjected to DNA
5 sequencing (Big Dye chemistry on an ABI377 sequencer, Applied Biosystems, Foster City, CA).

Plasmids exhibiting the correct DNA sequence were digested with BglII restriction enzyme and the BglII fragment was gel purified using a GeneClean II purification kit
10 (Bio101, Carlsbad, CA). The purified BglII fragment was cloned into the BamHI site of the expression vector pET9a. The pET9a/2086 clones were selected on Terrific Broth plates supplemented with 30 µg/ml kanamycin. Kanamycin resistant clones were grown and miniprep plasmid DNA was prepared. The plasmids were screened for the appropriate orientation of the 2086 gene in the BamHI site. Correctly oriented plasmids represent a
15 fusion of the T7-antigen to the amino terminus of 2086 gene (rP2086T7). These rP2086T7 gene fusions were transformed into BLR(DE3)pLysS, selected on Terrific Broth/Kan plates, grown in Terrific Broth and induced to express the rP2086T7 fusion protein with 1 mM IPTG (isopropyl β-D-thiogalactopyranoside). The rP2086T7 fusion protein expressed at high
20 levels.

These fusion plasmids were then subjected to a NdeI restriction digest, which deletes the T7-antigen and links the mature 2086 gene directly to the ATG start provided by the vector. These NdeI deleted plasmids were transformed into Top10 cells and selected on Terrific Broth/Kan plates. Candidate clones were grown and
25 miniprep plasmid DNA was prepared. The plasmid DNA was subjected to DNA sequencing to confirm the deletion and the integrity of the 2086 gene sequence. These plasmids are represented by the plasmid map designated pPX7328 (FIG. 6). Plasmids representing the correct DNA sequence were transformed into BLR(DE3)pLysS, selected on Terrific Broth/Kan plates, grown in Terrific Broth and
30 induced to express the 2086 protein with IPTG. The pET9a vector failed to express the mature 2086 protein, in strain BLR(DE3)pLysS, when the T7-Tag was removed.

Production of Non-lipidated 2086 protein:

Purified plasmid DNA was used to transform the expression strain BLR(DE3)pLysS. BLR(DE3)pLysS cells carrying the plasmids are resistant to kanamycin and can be induced to express high levels of PorA protein by the addition of 1 mM IPTG. The rP2086T7 fusion protein can be expressed as insoluble inclusion bodies in the *E.coli* cell line BLR(DE3)pLysS at ~40% of total protein. This purified fusion protein was used to immunize mice and generated significant levels of bactericidal antibodies against a heterologous meningococcal strain. (See Table V)

2086 Non-lipidated gene mutagenesis:

PCR primer mutagenesis was performed on the 5' end of the 2086 gene. Expression studies are under way to determine if the T7-Tag can be removed while exhibiting the high expression levels of mature rP2086T7.

Purification of non-lipidated rP2086T7:

E. coli BLR(DE3)pLysS cells expressing non-lipidated rP2086T7 were lysed by microfluidizer in 10mM Hepes-NaOH/5mM EDTA/1mM Pefabloc SC pH 7.4.

The cell lysate was then centrifuged at 18,000xg for 30 minutes. The inclusion body pellet was washed three times with 50mM Tris-HCl/5mM EDTA/1% TritonX-100 pH 8 followed by centrifugation each time at 24,000xg for 30 min. The inclusion body pellet was then washed twice with 50mM Tris-HCl/5mM EDTA/1% Zwittergent 3-14 pH 8 followed by centrifugation each time at 24,000xg for 15min. The inclusion body pellet was then solubilized with 50mM Tris-HCl/5mM EDTA/4M Urea pH 8 for two hours followed by centrifugation to remove insoluble material. The supernatant (solubilized rP2086T7) was split into four equal samples. One sample was adjusted to 50mM Tris-HCl/5mM EDTA/250mM NaCl/2M Urea pH8 (no detergent), one was adjusted to 50mM Tris-HCl/5mM EDTA/250mM NaCl/2M Urea/1% hydrogenated Triton X-100 pH8 (TX-100), one was adjusted to 50mM Tris-HCl/5mM EDTA/250mM NaCl/2M Urea/1% Zwittergent 3-12 pH8 (Z3-12), and one was

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adjusted to 50mM Tris-HCl/5mM EDTA/250mM NaCl/2M Urea/1% Zwittergent 3-14 pH8 (Z3-14) using stock solutions. To remove the urea, samples were dialyzed to completion against the respective buffer containing no urea. The samples were then dialyzed to completion against the respective buffer containing no urea and 60mM NaCl to reduce the NaCl concentration. Insoluble material was removed by centrifugation at 2,000xg for 15 minutes, and the resulting supernatant (refolded rP2086T7) was used for further experiments. Homogeneity of rP2086T7 was found to be 91-95% as determined using Coomassie stained SDS-PAGE and laser densitometry.

Immunogenicity Procedure – As described in Example 2

This purified fusion protein was used to immunize mice and generated significant levels of bactericidal antibodies against a heterologous meningococcal strain. (See Table V below):

TABLE V: Bactericidal titers of mouse antibody raised to rP2086T7

MOUSE SERUM	DESCRIPTION	HETEROLOGOUS STRAIN/ H44/76
AF780 week 6	r2086T7 , 10ug	3200
Week 0 pool	Pre-immune serum	10
AE203 week 6	rLP2086, 10 ug (positive control)*	6400

(* positive control sera generated by immunization of mice with rLP2086)

Example 4

Development of Chimeric Clones of ORF 2086

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The N-terminal region of the 2086 gene from strain CDC-1573 contains a repeated segment not present in the 2086 gene from strains 8529 and 2996 (see FIG. 8). It appears that this repeated segment is responsible for increased levels of recombinant 2086 protein expression from two *E.coli* based expression systems (pET and pBAD). The recombinant protein expression level from the CDC-1573 2086 gene was significantly better in the pET and pBAD expression systems as compared to the recombinant expression levels from the 2086 gene with strains 8529 and 2996 using the same systems. The N-terminal region of the 2086 gene from all three strains is relatively homologous, except for this repeated segment. Therefore, it is reasonable to assume that by fusing the CDC-1573 N-terminus to the 2086 genes from strains 8529 and 2996, that the recombinant 2086 protein levels expressed from these genes will increase when using the pET and pBAD systems.

Materials and Methods:

Chromosomal DNA from strains 8529 and 2996 was purified and used as a template for PCR amplification of the chimeric 2086 gene. PCR primers with the compound numbers 6721 and 5135 (SEQ ID NOS. 321 and 308, respectively) were used to amplify the chimeric 2086 gene from strain 8529 and PCR primers with the compound numbers 6721 and 6605 (SEQ ID NOS. 321 and 320, respectively) were used to amplify the chimeric 2086 gene from strain 2996. The PCR products were cloned directly into the PCR2.1 TOPO vector from Invitrogen and then screened by DNA sequence analysis to identify an intact chimeric 2086 gene. That gene was then cleaved from the PCR2.1 vector with BglII and the BglII fragment was inserted into the BamHI site of the pET9a plasmid. Plasmid inserts were screened for the appropriate orientation and then subjected to a NdeI digestion. The linear NdeI fragments were self-ligated to achieve the deletion of a small NdeI fragment containing the T7-tag sequence contributed by the pET9a vector. This deletion directly links the T7 promoter to the 5' end of the chimeric 2086 gene. The NdeI deleted plasmid was transformed into *E.coli* strain BL21(DE3) and kanamycin resistant colonies were screened for chimeric 2086 protein expression with IPTG induction.

Initial studies indicate that the chimeric 2086 gene from strain 2996 expresses about twice as much recombinant protein as compared to the native 2996/2086 gene when expressed in the pET9a system. The pBAD system has not been tested yet.

5

Although only one experiment has been performed, the data indicate that there is an enhanced utility from the chimeric 2086 gene. The generation of CDC-1573 N-terminal fusions to the 2086 genes from strains 8529 and 2996 provides enhanced recombinant 2086 protein expression.

10

Example 5

2086 PCR Screening of *N. meningitidis* strains:

In order to determine the conservation of the 2086 gene among clinical isolates, PCR amplification was performed on 88 *N. meningitidis* strains.

15

Initial PCR identification of ORF 2086 utilized primers listed in Table IV (see Example 2 above) identified by compound numbers: 4623, 4624 and 4625 (SEQ ID NOS. 303, 304 and 305, respectively). These primers were designed based on Sanger's *N. meningitidis* serogroup A sequence. To facilitate screening a large number of strains, internal primers were designed for the 2086 gene. A total of 88 *N. meningitidis* strains were screened by PCR with the newly designed internal 2086 primers identified by compound numbers 5005 and 5007 (SEQ ID NOS. 306 and 307). With these primers the applicants were able to identify the 2086 gene from 63 of the 88 (~70%) *N. meningitidis* strains, (see Table VI-A).

20

25

Expanded regions surrounding the 2086 gene in Sanger's *N. meningitidis* serogroup A sequence and TIGR's *N. meningitidis* serogroup B sequence were examined and aligned. Primers were designed to correspond to regions upstream and downstream of the 2086 gene. The purpose was to utilize these primers to amplify greater than full length 2086 genes from a variety of *N. meningitidis* strains for

sequence comparison. PCR amplification of one strain (6557), using Compound Nos. 6470 and 6472 (SEQ ID NOS: 313 and 314, respectively), resulted in a low yield of product. The strain 6557 amplified product was cloned and plasmid DNA was submitted for sequence analysis. Results indicated a new type of 2086 gene with greater sequence variability than had previously been seen. The 2086 gene from strain 6557 was ~75% identical at the amino acid level to the other strains sequenced. Interestingly, strain 6557 was one of the 30% of strains that had previously tested negative by 2086 PCR screening described above.

Internal primers specific to the C-terminal variable regions within strain 6557 were designed. These primers were used to screen for the more variable 2086 gene in the ~30% of strains that had previously tested negative by 2086 PCR screening. All available *N. meningitidis* strains (n = 88) were screened by PCR with these newly identified internal 2086 primers (identified by compound numbers 6495 and 6496; SEQ ID NOS. 159 and 160, respectively). Only the ~30% of *N. meningitidis* strains that had previously tested negative by PCR for 2086 were PCR positive in this screen. The set of genes amplified from the previously PCR negative (~30%) strains should represent a new type of 2086 gene or a second family of 2086 genes and herein are designated 2086 Subfamily A. The set of 2086 genes amplified from the ~70% of strains with the 8529 derived primers are herein designated Subfamily B.

Subfamily A of 2086 genes is exemplified by the odd numbered SEQ ID NOS:1-173 without limitation. Subfamily B of 2086 genes is exemplified, without limitation, by the odd numbered SEQ ID NOS: 175-251

N. meningitidis strains used for PCR amplification studies were selected from the following tables, Table VI-A and Table VI-B. The strains listed in the tables are provided as examples of *N. meningitidis* strains, without limitation. The strains listed in Table VI-A are classified in 2086 protein Subfamily A and the strains listed in Table VI-B are classified in 2086 protein Subfamily B. The strains listed in each table are grouped by serosubtype. The strains are available from the following four sources as indicated in the table: MPHL-Manchester Public Health Laboratory, Manchester, UK; RIVM, Bilthoven, The Netherlands; University of Iowa, College of

Medicine, Department of Microbiology, Iowa City, IA; and Walter Reed Army
Institute of Research, Washington, D.C.

TABLE VI-A

Strain	Serosubtype	Source
M97 251854	B:4z, PI:4	MPHL
M98 250622	B:2b, PI:10	MPHL
M98 250572	B:2b, PI:10	MPHL
M98 250771	B:4z, PI.22,14	MPHL
M98 250732	B:4z, PI.22,14a	MPHL
M98 250809	B:15, PI:7,16	MPHL
M97 252697	B:1, PI:6, P1.18,25	MPHL
M97 252988	B:4, PI:6, P1.18,25,6	MPHL
M97 252976	B:4, PI:6, P1.18,25	MPHL
M97 252153	B:4, PI:6, P1.18,25	MPHL
M97 253248	B:15,PI:7, NT, 16	MPHL
CDC1610	P1:NT 4(15), P1.18-7,16-14	CDC
CDC1521	P1.6,3 2b(4)	CDC
CDC1034	P1.7 4(15)	CDC
L8	P1.7,1 15(4)	Walter Reed
CDC1492	P1.7,1 4(15)	CDC
870446	P1.12a,13	RIVM
CDC2369	P1.(9),14	CDC
6557	P1.(9),14, P1.22a,14a	RIVM
2996	P1.5,2, P1.5a,2c	RIVM
NmB	P1.5,2, P1.5a,2c	UIOWA
L3	P1.5,2	Walter Reed
B16B6	P1.5,2	RIVM
CDC1135		CDC
L5	P1.NT, P1.21-6,1	Walter Reed
L4	P1.21,16	Walter Reed
W135		Walter Reed
C11	C:16,P1.7,1	CDC
Y		Walter Reed

TABLE VI-B

Strain	Serosubtype	Source
M98 250670	B:1, PI:4	MPHL
M98 250024	B:1, PI:4	MPHL
M97 253524	B:1, PI:4	MPHL
M97 252060	B:1, PI:4	MPHL
M97 251870	B:4z, PI:4	MPHL
M97 251836	B:4z, PI:4	MPHL
M97 251830	B:4z, PI:4	MPHL
M97 251905	B:4z, PI:4	MPHL
M97 251898	B:4z, PI:4	MPHL
M97 251885	B:4z, PI:4	MPHL
M97 251876	B:4z, PI:4	MPHL
M97 251994	B:4z, PI:4	MPHL
M97 251985	B:4z, PI:4	MPHL
M97 251957	B:4z, PI:4	MPHL
M97 251926	B:4z, PI:4	MPHL
M97 252045	B:4z, PI:4	MPHL
M97 252038	B:4z, PI:4	MPHL
M97 252026	B:4z, PI:4	MPHL
M97 252010	B:4z, PI:4	MPHL
M97 252098	B:4z, PI:4	MPHL
M97 252083	B:4z, PI:4	MPHL
M97 252078	B:4z, PI:4	MPHL
M98 250735	B:4z, PI:15	MPHL
M98 250797	B:4z, PI:15	MPHL
M98 250768	B:4z, PI:15	MPHL
M98 250716	B:2b, PI:10	MPHL
M98 250699	B:4z, PI:10	MPHL
M98 250393	B:4z, PI:10	MPHL
M98 250173	B:4z, PI:10	MPHL
M97 253462	B:4z, PI:14	MPHL
M98 250762	B:15, PI:7,16	MPHL
M98 250610	B:15, PI:7,16	MPHL
M98 250626	B:15, PI:7,16	MPHL
M97 250571	B:15, PI:16	MPHL
M97 252097	B:15, PI:16, P1.7b,16	MPHL
M97 253092	B:1, PI:6	MPHL
M97 252029	B:15, PI:7, NT	MPHL
M97 251875	B:15, PI:7, NT	MPHL

Strain	Serosubtype	Source
CDC1127	PI.7,16 4(15)	CDC
CDC982	PI.7,16 4(15)	CDC
CDC1359	PI.7,16 4(15)	CDC
CDC798	PI.7,16 15(4)	CDC
CDC1078	PI.7,16 15(4)	CDC
CDC1614	PI.7,16 15(4)	CDC
CDC1658	PI.7,16 15(4)	CDC
H44/76	PI.7,16 15(4)	RIVM
CDC1985	P1.7,13 4(15)	CDC
L6	P1.7,1 ?(4)	Walter Reed
CDC1573	P1.7,1 4(15)	CDC
L7	P1.7,(9),1	Walter Reed
CDC937	P1.7,3, P1.7b,3	CDC
8529	P1.7,3, P1.7b,3	RIVM
880049	P1.7b,4	RIVM
CDC2367	P1.15 4(15)	CDC
H355	P1.19,15	RIVM
CDC1343	P1.14 4(15)	CDC
M982	P1.22,9	RIVM
870227	P1.5c,10	RIVM
B40	P1.5c,10	RIVM
5315	P1.5c,10	RIVM
CDC983	P1.5,2	CDC
CDC852	P1.5,2	CDC
6940	P1.18,25 (6)	RIVM
A4		

Other strains are readily available as isolates from infected individuals.

Example 6

Reactivity of rLP2086 antisera against meningococcal strains:

- 5 The following table, Table VII, shows the cross-reactive and cross protection capacity of the rLP2086 as described above. As indicated in the table, the rLP2086 was processed and analyzed using a variety of techniques including whole cell ELISA (WCE) titers, bactericidal assay (BCA) and Infant Rat (IR) assays to determine the

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bacterial cell surface reactivity of a polyclonal antibody raised against the 2086 protein.

TABLE VII

Reactivity of rLP2086-8529 antisera against multiple meningococcal strains

Strain	Serosubtype	WCE	BC	IR
2086 Subfamily A				
870446	P1.12a,13	808,615	>800	
NmB	P1.5a,2c	47,954	<100	
6557	P1.22a,14a	169,479	<25	-
2086 Subfamily B				
880049	P1.7b,4	1,402,767	100	+
H44/76	P1.7,16	8,009,507	>6400	
H355	P1.19,15	10,258,475	3,200	+
6940	P1.18,25(6)	5,625,410	800	
870227	P1.5c,10	4,213,324	<25	+
252097	P1.7b,16	10,354,512	>800	
539/8529	P1.7b,3	11,635,737	3,200	
M982	P1.22,9	1,896,800	800	
CDC-1573	P1.7a,1	208,259	25	
CDC-937	P1.7b,(3)	9,151,863	>800	

+ greater than 10 fold reduction in bacteremia

5 - less than 10 fold reduction in bacteremia

Example 7

Various constructs for expressing ORF2086 protein were prepared. The following table, Table VIII, is an r2086 construct table which is provided for the

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purpose of showing examples and illustrating an implementation of the present invention, without limitation thereto.

TABLE VIII
r2086 Construct Summary

Construct	Promoter	Leader	Expression	Extraction	Vector	% total Protein
pPX7340	T7	native	Coomassie	sarcosyl soluble	pET27b	2.5% processed lipoprotein
pPX7341	T7	P4	Coomassie	sarcosyl soluble	pET27b	5% processed lipoprotein
pPX7343	Arabinose	P4	Coomassie	sarcosyl soluble	pBAD18 cm	7-10% processed lipoprotein
pPX7325	T7	T7-tag fusion/ mature	Coomassie	inclusion bodies	pET9a	40-50% mature protein
pPX7328	T7	mature	Coomassie	soluble	pET9a	10% mature protein

5 Example 8

Further studies with LOS depleted outer membrane proteins identified additional strains producing outer membrane protein(s) other than PorA which were capable of eliciting bactericidal antibodies to strains expressing heterologous serosubtypes. The following describes further studies to identify additional proteins according to one embodiment of the present invention, and specifically outer membrane lipoproteins, which can reduce the number of proteins required in a meningococcal immunogenic composition. These further studies supplement the studies described in the previous examples.

Subcellular fractionation, differential detergent extraction, isoelectric focusing, and ion exchange chromatography were used in conjunction with

immunization and bactericidal assays against multiple strains to identify small groups of proteins of interest. Direct sequencing of the main components indicated that the N-termini were blocked. Internal protein sequences were obtained by direct sequencing of polypeptides derived from chemical and proteolytic digests. The

5 genomic sequence of a group A meningococcal strain was downloaded from the Sanger Center and analyzed by our Bioinformatics group using existing and proprietary algorithms to create a searchable database. The peptide sequence data indicated that ORF2086 was of interest. Primers based on this orf were used to PCR the P2086 gene from strain 8529. Analysis of the gene sequence, the fact that the N-

10 terminus was blocked, and its subcellular location indicated that P2086 is a lipidated outer membrane protein(LP2086). rLP2086-8529 and variants from other meningococcal strains were recombinantly expressed as lipoproteins in E.coli using the *H.influenzae* P4 signal sequence. These recombinant proteins were isolated from E.coli membranes by differential detergent extraction, purified using ion exchange

15 chromatography, and used to immunize mice. Mouse anti-LP2086 sera were able to facilitate bactericidal activity against several different serosubtype strains of *N.meningitidis*. Further analysis of the P2086 genes from many *N. meningitidis* strains showed that these sequences fell into two groups designated Subfamily A and Subfamily B. (See FIG. 12) The antisera raised against the Subfamily B proteins

20 were bactericidal against nine strains expressing Subfamily B proteins, and one strain expressing a Subfamily A protein. Subfamily A antisera were bactericidal against Subfamily A strains. A mixture of one rPorA and one rLP2086 elicited complementary antibodies extending vaccine coverage beyond that induced by either protein alone.

25 These observations lead to the following conclusions. rLP2086 antigens are capable of eliciting bactericidal antibodies against meningococcal strains expressing heterologous PorAs and heterologous P2086 proteins. The P2086 family of antigens may be a useful vaccine or immunogenic either alone or in combination with other neisserial antigens.

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The following describes the foregoing study in detail. A complex mixture of soluble outer membrane proteins (sOMPs) was found to elicit PorA independent bactericidal antibody against strains expressing heterologous PorA proteins. A process of differential detergent extraction, isoelectric focusing and ion exchange chromatography followed by mouse immunization was used to follow the immunologically active components.

At each step, sera was assayed for surface reactivity and bactericidal activity against several strains containing serosubtype antigens that are representative of the worldwide epidemiology of meningococcal disease.

10 This process of separation and immunization was used to identify a novel cross-reactive immunogenic candidate for Group B *N. meningitidis*.

Generation of PorA deficient strains - The porA chromosomal locus was cloned into plasmid pPX7016 from strain 2996. Within the plasmid the porA promoter, the S/D box and the first 38 N-terminal codons have been deleted and replaced with a self contained KanR expressing cassette. The plasmids were linearized with restriction enzymes and naturally transformed into the serosubtype strains PI:5,2; PI:9; PI:7,16; PI:15; PI:4; PI:3 & PI:10. Kanamycin resistant transformants were selected and screened for the loss of PorA by serosubtype specific monoclonals in an ELISA.

20 Bactericidal Assay : See Mountzourous, K.T. and Howell, A.P. Detection of Complement-Mediated Antibody-Dependent Bactericidal Activity in a Fluorescence-Based Serum Bactericidal Assay for Group B *Neisseria meningitidis*. J Clin Microbiol. 2000;38:2878-2884.

Whole Cell Enzyme Linked Immunosorbant Assay (ELISA): *N. meningitidis* whole cell suspensions were diluted to an optical density of 0.1 at 620nm in sterile 0.01M phosphate, 0.137M NaCl, 0.002M KCl (PBS). From this suspension, 0.1mL were added to each well of Nunc Bac T 96 well plates (Cat# 2-69620). Cells were dried on the plates at 37°C overnight, then were covered, inverted and stored at 4°C.

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Plates were washed three times with wash buffer (0.01M Tris-HCl, 0.139M NaCl/KCl, 0.1% Brij-35, pH 7.0-7.4). Dilutions of antisera were prepared in PBS, 0.05% Tween-20/Azide and 0.1mL was transferred to the coated plates and incubated for two hours at 37°C. Plates were washed three times in wash buffer. Goat-anti-

5 mouse IgG AP (Southern Biotech) was diluted at 1:1500 in PBS/0.05% Tween-20, 0.1mL was added to each well, and plates were incubated at 37°C for two hours. Plates were washed (as above). Substrate solution was prepared by diluting p-nitrophenyl phosphate (Sigma) in diethanolamine at 1mg/ml. Substrate was added to the plate at 0.1mL per well and incubated at room temperature for one hour. The

10 reaction was stopped with 50ul/well of 3N NaOH and plates were read at 405nm with 690nm reference.

Recombinant PorA Induction: The BLR(DE3)/pET9a strains were grown overnight at 37°C in HySoy Broth (Sheffield Products) supplemented with Kan-30 and 2% glucose. In the morning the O/N cultures were diluted 1/20 in HySoy Broth

15 Kan-30 and 1% glycerol and grown at 37°C for 1 hour. These cultures were induced by the addition of IPTG to a final concentration of 1mM. The cultures were grown for an additional 2-3 hours and then harvested.

Recombinant PorA Purification: The rPorA was solubilized from *E. coli* inclusion bodies with 8M Urea, and refolded by dialysis against buffer containing no

20 urea. The refolded rPorA was then concentrated by diafiltration and buffer exchanged by G25 column into NaPO₄ pH6. The dialyzed rPorA was then run on a cation exchange column (S Fractogel) and eluted with 1M NaCl.

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The sOMPs from strain 8529 (P1.7-2,3) elicit PorA independent bactericidal activity in mice against strains expressing heterologous serosubtypes. The following table, Table IX, shows the bactericidal activity in the studied strains.

TABLE IX

Test Strain	Serosubtype	BC ₅₀ Titer ¹
539	P1.7-2,3	1280
539 PorA-	NST ²	1080
H44/76	P1.7,16	3285
H44/76 PorA-	NST	2620
H355	P1.19,15	>1350
H355 PorA-	NST	>1350
880049	P1.7-2,4	290
880049 PorA-	NST	85
M982	P1.22,9	85
M982 PorA-	NST	<50

5

Preparation of sOMPs: *N. meningitidis* membranes were extracted with TX-100, Zwittergent 3-14, and Zwittergent 3-14+0.5M NaCl. The sOMPs referred to above were solubilized in the Zwittergent 3-14/0.5M NaCl extract. The extraction is performed using techniques well known to persons skilled in the art, for example, see U.S. Patent No. 6,355,253 which is hereby incorporated by reference.

10

Immunogenicity: Female Swiss-Webster mice were immunized with 25ug total protein adjuvanted with 20ug QS-21 at week 0 and 4. An exsanguination bleed and data analysis were done at week 6.

¹ Bactericidal (BC₅₀) titers represented as the reciprocal of the dilution of anti-sera which reduces viable cell count by 50%. Week 0 normal mouse sera had BC₅₀ titers of <25

15

² NST = Non Serosubtypable

The following table, Table X, shows the purification and characterization summary for recombinant lipidated P2086 (rLP2086) for both Subfamily A and Subfamily B.

5 Subfamily A rLP2086 Purification

TABLE X

rLP2086 Variant	A.A. Homology (%) ¹	Theoretical pI	Purity (%) ²
870446	75	6.1	80
2996	71	5.9	95
M97 252988	71	6.3	96
C11	68	6.4	82
M98 250771	62	6.1	83

10 Subfamily B rLP2086 Purification

TABLE XI

rLP2086 Variant	A.A. Homology (%) ¹	Theoretical pI	Purity (%) ²
8529	100	7.5	96
M982	94	6.3	96
88049	92	6.2	90
CDC1573	87	5.6	93

Purification Method: All variants were solubilized from *E. coli* membranes with TX-100 (exception rLP2086-8529 which was solubilized with Sarcosyl or Urea).

- 15 Further purification was achieved with a combination of anion exchange (TMAE), size exclusion and/or cation exchange (S Fractogel) chromatography in a Tris-HCl or NaPO₄ buffer.

1 Amino acid homology as compared to P2086 from strain 8529

2 Purity as determined by SDS-PAGE and laser densitometry of colloidal

- 20 Coomassie stained band (Simply Blue stain)

Immunogenicity of a Subfamily B member, rLP2086-8529, tested against homologous and heterologous strains

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Table XII below shows immunogenicity of a Subfamily B member, rLP2086-8529, tested against homologous and heterologous strains

TABLE XII

Target Strain	P2086 Subfamily	Target Strain Serosubtype	A.A. Homology ^a	Whole Cell ELISA ^b Titer	BC ₅₀ Titer ^c
539	B	P1.7-2,3	100	>1,458,000	3,200
H44/76	B	P1.7,16	100	>1,458,000	3,200
H355	B	P1.19,15	100	>1,458,000	3,200
CDC937	B	P1.7-2,3-4	100	>1,458,000	>800
M97 252097	B	P1.7-2,16	100	>1,458,000	>800
870227	B	P1.5-2,10	100	>1,458,000	<25
6940	B	P1.18,25,6	97	900,162	>800
M982	B	P1.22,9	94	435,909	200
880049	B	P1.7-2,4	92	349,912	400
CDC1573	B	P1.7-1,1	87	102,508	25
870446	A	P1.12-1,13	71	389,829	800
M98 250771	A	P1.22,14	62	139,397	<25
NmB	A	P1.5-1,2-2	71	<2,000	<25

5 Vaccination Procedure: 6-8 week old female Swiss-Webster mice were immunized with 10ug rLP2086-8529+20ug QS-21 at week 0 and week 4. Data analysis was performed on the week 6 exsanguination bleed.

aAmino acid homology of P2086 as compared to rLP2086-8529

b Endpoint titers expressed as the reciprocal of the dilution at absorbance = 0.1

10 c BC50 titers represented as the reciprocal of the dilution of anti-sera which reduces viable cell count by 50%. Week 0 normal mouse sera had BC50 titers of <10

Table XIII shows immunogenicity of a Subfamily B member, rLP2086-2996, tested against homologous and heterologous strains.

TABLE XIII

Target Strain	P2086 Subfamily	Target Strain Serosubtype	A.A. Homology ^a	Whole Cell ELISA ^b Titer	BC ₅₀ Titer ^c
NmB	A	P1.5-1,2-2	99.6	8,979	<25
870446	A	P1.12-1,13	99	<1,458,000	>800
M97 252697	A	P1.18,25,6	98	320,732	>800
6557	A	P1.22-1,14-1	98	17,319	<25
M98 250732	A	P1.22,14-1	89	241,510	>800
M98 250771	A	P1.22,14	89	447,867	800
H44/76	B	P1.7,16	72	56,386	<25

Vaccination Procedure: 6-8 week old female Swiss-Webster mice were
 5 immunized with 10ug rLP2086-2996+20ug QS-21 at week 0 and week 4. Data analysis was performed on the week 6 exsanguination bleed.

aAmino acid homology of P2086 as compared to rLP2086-2996

b Endpoint titers expressed as the reciprocal of the dilution at absorbance = 0.1

c Bactericidal (BC50) titers represented as the reciprocal of the dilution of
 10 anti-sera which reduces viable cell count by 50%. Week 0 normal mouse sera had BC50 titers of <10.

Table XIV below shows that antisera to rLP2086 and rPorA are complimentary when mixed and assayed for bactericidal activity.

15

TABLE XIV

Antisera	H44/76 (P1.7,16)	NMB (P1.5-1,2-2)	880049 (P1.7-2,4)	H355 (P1.19,15)	870227 (P1.5-2,10)	6557 (P1.22-1,14-1)
Anti-rLP2086 + three rPorA antisera	>3,200	>800	200	>800	200	200
Controls						
anti-rLP2086	6,400	<25	100	3,200	<25	<25
Corresponding monovalent rPorA antisera	-	1,600	-	-	200	400

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Vaccination Procedure: 6-8 week old female Swiss-Webster mice were immunized with either 10ug rLP2086-8529/20ug QS-21, or 15ug rPorA/100ug MPL at week 0 and week 4. Data analysis was performed on the week 6 exsanguination bleed.

a Bactericidal (BC50) titers represented as the reciprocal of the dilution of anti-sera which reduces viable cell count by 50%. Week 0 normal mouse sera had BC50 titers of <10.

The following table, Table XV, shows that mixtures of rLP2086 Subfamilies and two rPorAs elicit bactericidal antibody in mice.

TABLE XV

	H44/76	6940	880049	M982	M98 250771	M98 250732	M97 252697	870446	NmB	6557
	SfB ^b	SfB	SfB	SfB	SfA ^b	SfA	SfA	SfA	SfA	SfA
	P1.7,16	P1.18 25,6	P1.7- 2,4	P1.22 ,9	P1.22,1 4	P1.22,1 4-1	P1.18,2 5,6	P1.12- 1,13	P1.5- 1,2-2	P1.22 -1,14- 1
Antigen										
rLP2086- 8529 + rLP2086- 2996	>800	>800	200	400	800	>800	>800	>800	-	<25
rLP2086- 8529 + rLP2086- 2996 + rP1.5-1,2-2 + rP1.22- 1,14-1	>800	800	100	200	400	400	>800	>800	>800	200
Monovalent Controls ^c	>800	>800	200	400	800	>800	>800	>800	>800	800

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Vaccination Procedure: 6-8 week old female Swiss-Webster mice were immunized with 10ug of each protein + 20ug QS-21 at week 0 and week 4. Data analysis was performed on the week 6 exsanguination bleed.

5 a Bactericidal (BC50) titers represented as the reciprocal of the dilution of anti-sera which reduces viable cell count by 50%. Week 0 normal mouse sera had BC50 titers of <10.

bSfA – Subfamily A, SfB – Subfamily B

cRelevant monovalent control: rLP2086-8529, rLP2086-2996, rP1.5-1,2-2 or rP1.22-1,14-1 antisera

10 The following summarizes the results of the above described studies. Anti-rLP2086 antisera is bactericidal against 13/16 test strains. Eleven strains expressing different serosubtypes are killed by anti-P2086 sera. Bactericidal activity of anti-rLP2086 sera is complimentary to anti-rPorA sera. Mixtures of P2086 and PorA elicit complimentary bactericidal antibodies in mice. Differential detergent extraction,
15 purification and immunization in conjunction with a functional antibody assay against many strains can be used to identify new vaccine candidates. P2086 has been identified as a vaccine candidate which elicits bactericidal antibody against strains heterologous in both P2086 and rPorA. Thus, the 2086 family of proteins may be a useful vaccine either alone or in combination with other neisserial antigens.

20

Example 9

In accordance with the previous examples, additional meningococcal strains, of varying serogroups, were screened by PCR for the presence of the ORF 2086 gene. Ultimately, one hundred meningococcal strains were screened. The following describes the
25 study and its overall results. These results supplement the data from the previous examples.

Two sets of internal PCR primers specific to the C-terminal variable regions were utilized to discriminate between Subfamily A and B gene sequences. The presence of a PCR

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amplified product of approximately 350 bp indicated that the 2086 gene sequence was present on the chromosome. All strains yielded a single PCR product of the expected size. The nucleotide sequences of fifty-five full-length ORF 2086 genes were determined, aligned (DNASTar MegAlign) and used to generate a phylogenetic tree. (See FIG. 12).

5

Nine of these 2086 genes were recombinantly expressed as a rLP2086 lipoprotein in a pBAD arabinose inducible promoter system and three of these genes were recombinantly expressed as a rP2086 non-lipidated protein in an IPTG inducible pET system. These recombinant proteins were expressed in E.coli B. The purified recombinant protein was used to immunize mice and the mouse antisera was assayed for its serum IgG titers and its bactericidal activity against a variety of heterologous meningococcal strains.

10

ORF 2086 was amplified by PCR from one of the following, whole meningococcal cells, purified chromosomal DNA or plasmid DNA templates.

15

Nine ORF 2086 genes were cloned into the vector pLP339, which fuses the *Haemophilus* P4 leader sequence to the 5' end of the ORF 2086 genes. E.coli strain BLR was used as the host strain for recombinant expression of the lipidated form of rP2086 from the pBAD/ORF 2086 clones. (See FIG. 10A) The pBAD arabinose inducible promoter drives the expression the P4 signal/ORF 2086 fusion protein to express a lipidated form of rP2086. Three P2086 genes, lacking a signal sequence, were cloned into a pET9a vector behind the highly active T7 phage promoter. E.coli strain BL21(DE3) was used as the host strain for recombinant expression of a non-lipidated form of ORF 2086 from the pET9a/ORF 2086 clones. (See FIG. 10B) The DE3 lysogen in E.coli strain BL21 can be induced to express the T7 RNA polymerase under the control of the lacUV5 promoter by addition of IPTG. See, WCE; FEMS Micro. Lett., 48 (1987) 367-371 and BCA; J. Clin. Microbiol., 38 (2000) 2878-2884.

20

25

The gene, ORF2086, was cloned and sequenced from fifty-five different *N. meningitidis* strains. The nucleotide sequences were aligned (DNASTar MegAlign) and used to generate a phylogenetic tree. (See FIG. 12). This tree reveals two distinct subfamilies of

30

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the ORF 2086 gene nucleotide sequence. The two subfamilies of genes are similar at their 5' ends, but contain considerable variation near their 3' ends. Although there appears to be significant variability, certain key regions of the gene are highly homologous amongst the different strains. These conserved regions may provide functional continuity for the protein and may be indicative of cross-protective epitopes to be exploited as vaccine targets.

The 2086 gene was cloned from several serogroup B meningococcal strains and expressed with and without the lipidation signal sequence. Referring to FIGS. 11A and 11B, gel photographs show the whole cell lysates of E.coli B expressing the r2086 protein. The non-lipidated form fused to the T7-Tag expressed at the highest level. The T7-Tag sequence may provide stability to the mRNA and significantly enhances the level of polypeptide translated. This fusion protein appears to deposit in inclusion bodies and can be purified and refolded readily with known protocols. The lipidated and non-lipidated forms of P2086 are expressed at approximately 5 to 8% of total cellular protein, with the exception of the T7-Tag fusions, which express rP2086 as approximately 50% of total protein. The non-lipidated form of the protein appears to be soluble and localized in the cytoplasm. The lipidated form of the protein appears to be associated with the membrane fractions and is solubilized with detergent.

The recombinant lipidated 2086 protein from *N. meningitidis* B strain 8529 consistently elicits greater serum IgG titers than the non-lipidated form (see Table XVI below), which correlates well with the enhanced level of bactericidal activity against both homologous and heterologous meningococcal strains (see Table XVII below). The protein in its native lipidated form may have superior tertiary structure for antigen presentation and/or the attached lipid may act as an adjuvant stimulating a greater immunogenic response.

TABLE XVI

Immune Response Elicited at Week 6 by WCE using
8529 rP2086 (non-lipidated) vs. 8529 rLP2086 (lipidated)

Mouse Sera		Meningococcal Strains				
Antigen	Adjuvant	H44/76	H355	870227	880049	870446

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(10 ug)	(20 ug)					
rP2088	QS-21	273,238	212,947	102,694	69,124	21,466
rLP2086	QS-21	5,384,306	4,819,061	2,930,946	1,307,091	886,056

TABLE XVII

8529 rP2086 Elicits Weaker Bactericidal Activity than 8529 rLP2086

5

Mouse Sera		Meningococcal Strains			
Antigen (10 ug)	Adjuvant (20 ug)	H44/76	H355	880049	NMB
rP2086	QS-21	200	100	<25	<25
rLP2086	QS-21	6,400	3,200	100	<25
Pre-Immune	-	<10	<10	<10	<10
Positive Control	-	1,600	100	200	1,600

The following is a summary of the results of the study. All *N. meningitidis* B strains tested appear to have one 2086-like gene. At least two families of the 2086 gene are represented:

- 10 Subfamily A - about 30% of strains and Subfamily B - about 70% of strains. The 2086 gene has been cloned and sequenced from 55 *N. meningitidis* strains. Sequences within Subfamily A are ~86-100% identical at the DNA level. Sequence within Subfamily B are ~89.5-100% identical at the DNA level. Sequences within Subfamily A vs. Subfamily B ~60.9%-74% identical at the DNA level. 2086 homologs have been identified by PCR screening in the
- 15 following:

N. meningitidis A, B, C, W135, Y

N. lactamica

N. gonorrhoeae FA1090

20

Several ORF 2086 genes have been cloned and recombinantly expressed

Lipidated versions of P2086 were expressed from nine meningococcal strains.

These recombinant proteins have been purified and used to vaccinate mice.

The resulting antisera is bactericidal.

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Non-lipidated versions of P2086 were expressed from three of the above nine strains. rLP2086 consistently elicits a greater immune response than rP2086. rLP2086 also exhibits enhanced bactericidal activity against both homologous and heterologous meningococcal strains.

5

Example 10

The following tables, Tables XVIII and XIX, show the characterization of variants of members of the two subfamilies.

10

TABLE XVIII
Subfamily A rLP2086 Variants -
Characterization

		rLP2086- 252988	rLP2086- 250771	rLP2086- 870446	rLP2086- 2996	rLP2086- C11
Growth Media		HySoy	HySoy	HySoy	HySoy	HySoy
Solubility		rTX-100 ⇒ Z3-12	TX-100	TX-100	rTX-100 ⇒ Z3-12	rTX-100 ⇒ Z3-12
Purification Steps		TMAE S Fractogel SEC	HQ Poros SEC	HQ Poros SEC	TMAE SEC	TMAE S Fractogel
Purity (%)		96	83	80	95	82
Yield (mg/g cell pellet)		0.2	0.7	0.8	0.5 (fermentor)	0.1
Size	SEC (Z3- 12)	134,000	155,000	132,000	163,000	126,000
	MS	27,897 (712 lipid)	-	-	27,878 (750 lipid)	28,139 (682 lipid)
Thermal Denaturation Transition Midpoint (T_M) °C		66 °C	-	NT	65 °C	63 °C
Protein Available		2.7mg	1mg (Z3-12)	5.0mg	44mg	1.1mg

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(mg)					
8529 Sequence Homology (%)	71	62	71	72	68

TABLE XIX
Subfamily B rLP2086 Variants -
Characterization

		rLP2086- 8529	rLP2086- M982	rLP2086- 880049	rLP2086- CDC1573
Growth Media		Apollon (Sanford)	Apollon	HySoy	HySoy
Solubility		4M Urea \Rightarrow Z3-12	rTX-100 \Rightarrow Z3-12	rTX-100 \Rightarrow Z3- 12	rTX-100
Purification Steps		TMAE S Fractogel	TMAE S Fractogel	TMAE S Fractogel	TMAE SEC
Purity (%)		96	96	90	93
Yield (mg/g cell pellet)		0.2 (fermentor)	1.6 (fermentor)	0.4	1.0
Size	SEC (Z3-12)	95,000	110,000 150,000	100,000	120,000
	MS	27,785 (822 lipid)	27,719 (711 lipid)	28,044 (819 lipid)	28,385 (823 lipid)
Thermal Denaturation Transition Midpoint (T_M) °C		70 °C	75 °C	62 °C	NT
Protein Available (mg)		Urea – 34mg Sarc – 36mg	Pool 1 – 47mg Pool 2 – 17mg	3.6mg	4.9mg
8529 Sequence Homology (%)		100	94	92	87

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Table XX below provides the results of fluorescent serum bactericidal assays for the 2086 Subfamily A.

TABLE XX

5

Description	250771	870446	6557	NMB	M98 250732	M97 252697
rLP2086-252988, 10µg	>800 (99%)*	>800 (99%)*	<25	-	>800 (99%)*	>800 (93%)*
rLP2086-C11, 10µg	200	>880 (91%)*	<25	-	200	400
rLP2086-250771, 10µg	>800 (92%)*	>800 (99%)*	<25	-	>800 (96%)*	>800 (84%)*
rLP2086-870446, 10µg	400	>800 (99%)*	<25	-	400	400
rLP2086-2996, 10µg	800	>800 (99%)*	<25	-	>800 (93%)*	>800 (72%)*
rLP2086-8529 + rLP2086-2996, 10µg	800	>800 (99%)*	<25	-	>800 (80%)*	>800 (72%)*
rLP2086-8529 + rP1.22a,14a + rP1.5a,2c, 10µg	-	800	200	>800 (98%)*	-	-
rLP2086-8529 + rLP2086-2996 + rP1.22a,14a + rP1.5a,2c, 10µg	400	>800 (99%)*	200	>800 (99%)*	400	>800 (88%)*
NMB/rLP2086- 8529 vesicles, 20µg	-	100	-	400	-	-
rP1.22a,14a, 10µg	25	-	800	-	100	-
rP1.5a,2c, 10µg	-	-	-	>800 (99%)*	-	-
rLP2086-8529, 10µg	-	800	-	-	-	-
rP1.22a,14a, 25µg	200	-	-	-	800	-
rP1.18,25.6, 5µg	-	-	-	-	-	-
nP1.22,9 (M982), 25µg	-	-	100	-	-	-
pre-immune mouse serum (negative control)	<10	<10	<10	<10	<10	<10
	800	400	800	1600	**	**

Notes:

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* Percentage indicates the % BC activity at the 1:800 dilution.

** Positive control not available.

– serum not tested

5

Example 11

The following further demonstrates that P2086 is expressed in neisserial strains and provides additional specific examples of P2086 expression in several strains.

Cell lysates were prepared with cells from plate cultures resuspended in SDS sample buffer and heated at 98°C for four minutes. Samples were loaded at ~30-50ug total protein per well on 10-20% pre-cast gels (ICN) and run at 175V. The gels were transferred to a nitrocellulose membrane, which was then blocked for 30min. with 5% powdered milk in Tris-buffered saline (Blotto). The primary antibody used was a pool of polyclonal antisera raised against individual rLP2086 variants in mice.

Referring to FIGS. 17 and 18, a Western Blot shows the reactivity of rLP2086 mouse antisera to P2086 Subfamily A and B whole cell lysates. For the Subfamily A cell lysate blot, the antisera used were raised against rLP2086-2996, -870446 and -250771 with rLP2086-250771 diluted at 1/500 in Blotto and the others diluted at 1/1000 in Blotto. For the Subfamily B cell lysate blot, the antisera used were raised against rLP2086-8529 (diluted 1/1000 in Blotto), -CDC1573, -M982 and -880049 (these three diluted 1/500 in Blotto). The primary antisera and blot were incubated at 4°C overnight. The blot was washed, a goat-anti-mouseAP secondary was added at 1/500 in Blotto, and the blot was incubated for 30min. at room temperature. After washing, the blot was developed using the BCIP/NBT Membrane Phosphatase Substrate System (KPL).

30

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The invention now being fully described, it will be apparent to one of ordinary skill in the art that many changes and modifications can be made thereto without departing from the spirit or scope of the invention as set forth herein. The foregoing describes the preferred embodiments of the present invention along with a number of possible alternatives. These embodiments, however, are merely for example and the invention is not restricted thereto.

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What is claimed is:

1. A composition comprising:

(a) at least one protein encoded by an open reading frame of *Neisseria species* (ORF2086), said open reading frame encoding a crossreactive immunogenic antigen, and said crossreactive immunogenic antigen providing immunogenicity against infection by *Neisseria meningitidis* serogroup B in a subject; or

(b) at least one immunogenic portion of at least one protein described in (a); or

(c) at least one biological equivalent of at least one protein described in (a) or immunogenic fragment described in (b).

2. The composition of claim 1, wherein the at least one protein comprises any of the amino acid sequences of SEQ ID NOS:254 to 259.

3. The composition of claim 1, wherein the at least one protein is encoded by ORF2086 in any of nesserial strains L3 6275, CDC2369, CDC1034, L4 891, B16B6, W135 (ATCC35559), C11, Y(ATCC35561), M98 250732, M98 250771, CDC1135, M97 252153, CDC1610, CDC1492, L8 M978; M97 252988, M97 252697, 6557, 2996, M97 252976, M97 251854, CDC1521, M98 250622, 870446, M97 253248, M98 250809, L5 M981, NMB or M98 250572.

4. The composition of claim 1, wherein the at least one protein comprises any of the amino acid sequences of SEQ ID NOS:260 to 278 or 279 to 299.

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5. The composition of claim 1, wherein the at least one protein is encoded by ORF2086 in any of nesserial strains 880049, M982, CDC1573, M97 253524 or M98 250670.

5 6. The composition of claim 1, wherein the at least one protein comprises the amino acid sequence of any of even numbered SEQ ID NOS:2-174.

7. The composition of claim 6, additionally comprising at least one protein comprising the amino acid sequence of any of even numbered SEQ ID
10 NOS:176-252.

8. The composition of claim 1, wherein the at least one protein comprises the amino acid sequence of any of even numbered SEQ ID NOS:224-252.

15 9. The composition of claim 1, wherein said at least one protein, immunogenic portion or biological equivalent is nonpathogenic and substantially free from any infectious impurities.

10 10. The composition of claim 1, wherein the at least one protein has a molecular weight of about 26,000 to about 30,000 daltons as measured by mass spectroscopy.

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11. The composition of claim 10, wherein the at least one protein has a molecular weight of about 28-35 kDa as measure on a 10%-20% SDS polyacrylamide gel.

5 12. The composition of claim 1, wherein said composition additionally comprises a pharmaceutically acceptable buffer, diluent, adjuvant or carrier.

13. The composition of claim 1, wherein said composition additionally comprises a carrier.

10

14. The composition of claim 1, wherein said composition additionally comprises an adjuvant.

15 15. The composition of claim 14, wherein said adjuvant comprises a liquid.

16. The composition of claim 1, wherein the protein is a recombinant protein.

20 17. The composition of claim 1, wherein the protein is isolated from native *Neisseria species*.

18. The composition of claim 1, wherein the protein is a lipoprotein.

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19. The composition of claim 1, wherein the protein is non-lipidated.

20. The composition of claim 1, wherein the composition additionally
5 comprises at least one PorA, PorB, transferrin binding protein, or opacity protein (Opc).

21. The composition of claim 1, wherein the composition additionally
comprises at least one additional surface antigen of *Neisseria species*, said additional
10 surface antigen being a non-ORF2086 protein.

22. The composition of claim 1, wherein said composition additionally
comprises a polysaccharide.

15 23. The composition of claim 1, wherein said composition comprises an
additional peptide, polypeptide or protein, said composition forming a conjugate that
induces an immune response to two or more bacteria in a mammal.

24. A composition comprising:

20 at least one immunogenic protein or polypeptide comprising any of SEQ ID
NOS: 254-259.

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25. The composition of claim 24, wherein the at least one protein has a molecular weight of about 26,000-30,000 daltons as measure by mass spectroscopy.

26. The composition of claim 25, wherein the at least one protein has a
5 molecular weight of about 28-35 kDa as measured on a 10%-20% SDS polyacrylamide gel.

27. The composition of claim 24, wherein said composition additionally comprises a pharmaceutically acceptable buffer, diluent, adjuvant or carrier.

10

28. The composition of claim 24, wherein said composition additionally comprises a carrier.

29. The composition of claim 24, wherein said composition additionally
15 comprises an adjuvant.

30. The composition of claim 29, wherein said adjuvant comprises a liquid.

20 31. The composition of claim 24, wherein the protein is non-lipidated.

32. The composition of claim 24, wherein the protein is a recombinant protein.

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33. The composition of claim 24, wherein the protein or polypeptide is isolated from native *Neisseria species*.

5 34. The composition of claim 24, wherein the protein is a lipoprotein.

35. The composition of claim 24, wherein the composition additionally comprises at least one PorA, PorB, transferrin binding protein, or opacity protein (Opc).

10

36. The composition of claim 24, wherein the composition additionally comprises at least one additional surface antigen of *Neisseria species*, said additional surface antigen being a non-ORF2086 protein.

15 37. The composition of claim 24, wherein said composition additionally comprises a polysaccharide.

38. The composition of claim 24, wherein said composition comprises an additional peptide, polypeptide or protein, said composition forming a conjugate that
20 induces an immune response to two or more bacteria in a mammal.

39. A composition comprising:

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at least one immunogenic protein or polypeptide comprising any of SEQ ID NOS:260 to 278.

40. The composition of claim 39, wherein said composition additionally
5 comprises a pharmaceutically acceptable buffer, diluent, adjuvant or carrier..

41. A composition comprising:

at least one immunogenic protein or polypeptide comprising any of SEQ ID NOS:279 to 299.

10

42. The composition of claim 41, wherein said composition additionally comprises a pharmaceutically acceptable buffer, diluent, adjuvant or carrier..

43. A composition comprising:

15 at least one isolated protein comprising the amino acid sequence of SEQ ID NO:300;

wherein x is any amino acid;

wherein the region from amino acid position 5 to amino acid position 9 is any of 0 to 5 amino acids;

20 wherein the region from amino acid position 67 to amino acid position 69 is any of 0 to 3 amino acids; and

wherein amino acid position 156 is any of 0 to 1 amino acid.

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44. The composition of claim 43, wherein the region from amino acid position 5 to amino acid position 9 comprises 0, 4 or 5 amino acids.

5 45. The composition of claim 43, wherein the region from amino acid position 67 to amino acid position 69 comprises 0 or 3 amino acids

46. The composition of claim 43, wherein the at least one protein has a molecular weight of about 26,000 to 30,000 daltons as measured by mass spectroscopy.

10

47. The composition of claim 46, wherein the at least one protein has a molecular weight of about 28-35 kDa as measured on a 10%-20% SDS polyacrylamide gel.

15 48. The composition of claim 43, wherein said composition additionally comprises a pharmaceutically acceptable buffer, diluent, adjuvant or carrier.

49. The composition of claim 43, wherein said composition additionally comprises a carrier.

20

50. The composition of claim 43, wherein said composition additionally comprises an adjuvant.

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51. The composition of claim 50, wherein said adjuvant comprises a liquid.

52. The composition of claim 43, wherein the protein is non-lipidated.

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53. The composition of claim 43, wherein the protein is a recombinant protein.

54. The composition of claim 43, wherein the protein is isolated from native *Neisseria species*.

10

55. The composition of claim 43, wherein the protein is a lipoprotein.

56. The composition of claim 43, wherein the composition additionally comprises at least one Por A, Por B, transferrin binding protein, or opacity protein (Opc).

15

57. The composition of claim 43, wherein the composition additionally comprises at least one additional surface antigen of *Neisseria species*, said additional surface antigen being a non-ORF2086 protein.

20

58. The composition of claim 43, wherein said composition additionally comprises a polysaccharide.

59. The composition of claim 43, wherein said composition comprises an additional peptide, polypeptide or protein, said composition forming a conjugate that induces an immune response to two or more bacteria in a mammal.

5

60. A composition comprising:

(a) at least one protein comprising the amino acid sequence of any of even numbered SEQ ID NOS:2-252;

10 (b) at least one protein encoded by a polynucleotide that hybridizes under stringent conditions to a polynucleotide comprising the nucleic acid sequence of any of odd numbered SEQ ID NOS:1-253;

(c) at least one immunogenic portion of at least one protein described in (a) or (b); or

15 (d) at least one biological equivalent of at least one protein described in (a) or (b) or immunogenic fragment described in (c).

61. The composition of claim 60, wherein the at least one protein comprises the amino acid sequence of any of even numbered SEQ ID NOS:2-174.

20 62. The composition of claim 61, additionally comprising at least one protein comprising the amino acid sequence of any of even numbered SEQ ID NOS:176-252.

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63. The composition of claim 60, wherein the at least one protein comprises the amino acid sequence of any of even numbered SEQ ID NOS:2-12.

5 64. The composition of claim 60, wherein the at least one protein comprises the amino acid sequence of any of even numbered SEQ ID NOS:14-24.

65. The composition of claim 60, wherein the at least one protein comprises the amino acid sequence of any of even numbered SEQ ID NOS:26-42.

10 66. The composition of claim 60, wherein the at least one protein comprises the amino acid sequence of any of even numbered SEQ ID NOS:50-60.

67. The composition of claim 60, wherein the at least one protein comprises the amino acid sequence of any of even numbered SEQ ID NOS:62-108.

15

68. The composition of claim 60, wherein the at least one protein comprises the amino acid sequence of any of even numbered SEQ ID NOS:110-138.

20 69. The composition of claim 60, wherein the at least one protein comprises the amino acid sequence of any of even numbered SEQ ID NOS:140-156.

70. The composition of claim 60, wherein the at least one protein comprises the amino acid sequence of any of even numbered SEQ ID NOS:158-174.

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71. The composition of claim 60, wherein the at least one protein comprises the amino acid sequence of any of even numbered SEQ ID NOS: 224-252.

5 72. The composition of claim 60, wherein the composition additionally comprises at least one Por A, Por B, transferrin binding protein, or opacity protein (Opc).

10 73. The composition of claim 60, wherein the composition additionally comprises at least one additional surface antigen of *Neisseria species*, said additional surface antigen being a non-ORF2086 protein.

74. The composition of claim 60, wherein the at least one protein has a molecular weight of about 26,000 to about 30,000 as measured by mass spectroscopy.

15

75. The composition of claim 74, wherein the at least one protein has a molecular weight of about 28-35 kDa as measured on a 10%-20% SDS polyacrylamide gel.

20 76. The composition of claim 60, wherein said composition additionally comprises a pharmaceutically acceptable buffer, diluent, adjuvant or carrier.

77. The composition of claim 60, wherein said composition additionally comprises a carrier.

78. The composition of claim 60, wherein said composition additionally comprises an adjuvant.

5 79. The composition of claim 78, wherein said adjuvant comprises a liquid.

80. The composition of claim 60, wherein the protein is non-lipidated.

10 81. The composition of claim 60, wherein the protein is a recombinant protein.

82. The composition of claim 60, wherein the protein is isolated from native *Neisseria species*.

15

83. The composition of claim 60, wherein the protein is a lipoprotein.

84. The composition of claim 60, wherein said composition additionally comprises a polysaccharide.

20

85. The composition of claim 60, wherein said composition comprises an additional peptide, polypeptide or protein, said composition forming a conjugate that induces an immune response to two or more bacteria in a mammal.

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86. A composition comprising:

at least one antigen of a first bacterial strain of *Neisseria species* that provides immunogenicity against infection of a subject by a second bacterial strain of *Neisseria species*.

5

87. The composition of claim 86, wherein the first strain is a strain of *Neisseria species* and said second strain is a strain of *Neisseria meningitidis* serogroup B.

10

88. The composition of claim 86, wherein the first strain is any of strains L3 6275, CDC2369, CDC1034, L4 891, B16B6, W135 (ATCC35559), C11, Y(ATCC35561), M98 250732, M98 250771, CDC1135, M97 252153, CDC1610, CDC1492, L8 M978; M97 252988, M97 252697, 6557, 2996, M97 252976, M97 251854, CDC1521, M98 250622, 870446, M97 253248, M98 250809, L5 M981, NMB or M98 250572.

15

89. The composition of claim 86, wherein the first strain is any of strains 880049, M982, CDC1573, M97 253524 or M98 250670.

20

90. The composition of claim 86, wherein the protein is a recombinant protein.

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91. The composition of claim 86, wherein the protein is isolated from native *Neisseria species*.

92. The composition of claim 86, wherein the protein is a lipoprotein.

5

93. The composition of claim 86, wherein said composition additionally comprises a pharmaceutically acceptable buffer, diluent, adjuvant or carrier.

10 94. The composition of claim 86, wherein said composition additionally comprises a carrier.

95. The composition of claim 86, wherein said composition additionally comprises an adjuvant.

15 96. The composition of claim 95, wherein said adjuvant comprises a liquid.

97. The composition of claim 86, wherein the protein is non-lipidated.

20 98. The composition of claim 86, wherein said composition additionally comprises a polysaccharide.

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99. The composition of claim 86, wherein said composition comprises an additional peptide, polypeptide or protein, said composition forming a conjugate that induces an immune response to two or more pathogens in a mammal.

5 100. A composition comprising:

at least one isolated protein comprising the amino acid sequence of SEQ ID NO:301;

wherein x is any amino acid;

10 wherein the region from amino acid position 5 to amino acid position 8 is any of 0 to 4 amino acids;

wherein the region from amino acid position 66 to amino acid position 68 is any of 0 to 3 amino acids.

15 101. The composition of claim 100, wherein the at least one protein has a molecular weight of about 26,000 to about 30,000 as measured by mass spectroscopy.

102. The composition of claim 101, wherein the at least one protein has a molecular weight of about 28-35 kDa as measured on a 10%-20% SDS polyacrylamide gel.

20

103. The composition of claim 100, wherein said composition additionally comprises a pharmaceutically acceptable buffer, diluent, adjuvant or carrier.

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104. The composition of claim 100, wherein said composition additionally comprises a carrier.

105. The composition of claim 100, wherein said composition additionally
5 comprises an adjuvant.

106. The composition of claim 105, wherein said adjuvant comprises a liquid.

107. The composition of claim 100, wherein the protein is non-lipidated.
10

108. The composition of claim 100, wherein the protein is a recombinant protein.

109. The composition of claim 100, wherein the protein is isolated from
15 native *Neisseria species*.

110. The composition of claim 100, wherein the protein is a lipoprotein.

111. The composition of claim 100, wherein said composition additionally
20 comprises a polysaccharide.

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112. The composition of claim 100, wherein said composition comprises an additional peptide, polypeptide or protein, said composition forming a conjugate that induces an immune response to two or more bacteria in a mammal.

5 113. The composition of claim 100, wherein the region from amino acid position 5 to amino acid position 8 comprises 0 or 4 amino acids

114. The composition of claim 100, wherein the region from amino acid position 66 to amino acid position 68 comprises 0 or 3 amino acids.

10

115. A composition comprising:

at least one isolated protein comprising the amino acid sequence of SEQ ID NO:302;

wherein x is any amino acid;

15 wherein the region from amino acid position 8 to amino acid position 12 is any of 0 to 5 amino acids.

116. The composition of claim 115, wherein the region from amino acid position 8 to amino acid position 12 comprises 0 or 5 amino acids.

20

117. The composition of claim 115, wherein the at least one protein has a molecular weight of about 26,000 to about 30,000 as measured by mass spectroscopy.

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118. The composition of claim 117, wherein the at least one protein has a molecular weight of about 28-35 kDa as measured on a 10%-20% SDS polyacrylamide gel.

5 119. The composition of claim 115, wherein said composition additionally comprises a pharmaceutically acceptable buffer, diluent, adjuvant or carrier.

120. The composition of claim 115, wherein said composition additionally comprises a carrier.

10 121. The composition of claim 115, wherein said composition additionally comprises an adjuvant.

122. The composition of claim 121, wherein said adjuvant comprises a liquid.

15

123. The composition of claim 115, wherein the protein is non-lipidated.

124. The composition of claim 115, wherein the protein is a recombinant polypeptide.

20

125. The composition of claim 115, wherein the protein is isolated from a natural source.

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126. The composition of claim 115, wherein said composition additionally comprises a polysaccharide.

127. The composition of claim 115, wherein said composition comprises an additional peptide, polypeptide or protein, said composition forming a conjugate that induces an immune response to two or more bacteria in a mammal.

128. A composition comprising:

at least one antibody that immunospecifically binds with any of:

- 10 (a) at least one protein encoded by an open reading frame of *Neisseria species* (ORF2086), said open reading frame encoding a crossreactive immunogenic antigen, and said crossreactive immunogenic antigen providing immunogenicity against infection by *Neisseria meningitidis* serogroup B in a subject; or
- 15 (b) at least one immunogenic portion of at least one protein described in (a); or
- (c) at least one biological equivalent of at least one protein described in (a) or one immunogenic fragment described in (b).

129. The composition of claim 128, wherein the antibody is a monoclonal antibody.

130. The composition of claim 128, additionally comprising a pharmaceutically acceptable carrier.

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131. A composition comprising:

at least one antibody that immunospecifically binds with any of:

(a) at least one protein comprising any of SEQ ID NOS:254 to 259; or

(b) at least one immunogenic portion of at least one protein described in

5 (a); or

(c) at least one biological equivalent of at least one protein described in (a) or one immunogenic fragment described in (b).

132. The composition of claim 131, wherein the at least one protein,
10 immunogenic portion thereof or biological equivalent thereof comprises any of SEQ ID NOS:260-299.

133. The composition of claim 131, wherein the at least one antibody is a monoclonal antibody.

15

134. A composition comprising:

at least one antibody that immunospecifically binds with at least one isolated protein comprising the amino acid sequence of SEQ ID NO:300;

wherein x is any amino acid;

20 wherein the region from amino acid position 5 to amino acid position 9 is any of 0 to 5 amino acids;

wherein the region from amino acid position 67 to amino acid position 69 is any of 0 to 3 amino acids; and

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wherein amino acid position 156 is any of 0 to 1 amino acid.

135. The composition of claim 134, wherein the at least one antibody is a monoclonal antibody.

5

136. A composition comprising:

at least one antibody that immunospecifically binds with any of:

(a) at least one protein comprising the amino acid sequence of any of even numbered SEQ ID NOS:2-252; or

10 (b) at least one protein encoded by a polynucleotide that hybridizes under stringent conditions to a polynucleotide comprising the nucleic acid sequence of any of odd numbered SEQ ID NOS:1-253;

(c) at least one immunogenic portion of at least one protein described in (a) or (b); or

15 (d) at least one biological equivalent of at least one protein described in (a) or (b) or immunogenic fragment described in (c).

137. A composition comprising:

20 at least one polynucleotide that (a) encodes at least one protein encoded by an open reading frame of *Neisseria species* (ORF2086) or at least one immunogenic portion or biological equivalent of said at least one protein, said open reading frame encoding a crossreactive immunogenic antigen, and said crossreactive immunogenic antigen providing immunogenicity against infection by *Neisseria meningitidis*

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serogroup B in a subject; or (b) hybridizes under stringent conditions to any of the polynucleotides described in (a).

138. The composition of claim 137, additionally comprising a P4 leader
5 sequence (SEQ ID NO. 322).

139. The composition of claim 137, wherein said composition comprises a
vector.

10 140. The composition of claim 139, wherein the vector is a plasmid.

141. The composition of claim 139, wherein the vector is a phage.

142. The composition of claim 137, wherein the stringent conditions are
15 high stringency southern hybridization conditions.

143. The composition of claim 137, further comprising a P4 leader
sequence (SEQ ID NO. 322).

20 144. The composition of claim 137, wherein the polynucleotide is a
recombinant polynucleotide.

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145. The composition of claim 137, wherein the polynucleotide is isolated from a natural source.

146. The composition of claim 137, wherein said composition additionally
5 comprises a nucleic acid sequence encoding for an additional peptide, polypeptide or protein.

147. A composition comprising:

at least one polynucleotide that (a) encodes at least one isolated protein
10 comprising any of SEQ ID NOS:254-259, 260-278 or 279-299, or (b) hybridizes under stringent conditions to any of the polynucleotides described in (a).

148. The composition of claim 147, additionally comprising a P4 leader sequence (SEQ ID NO. 322).

15

149. The composition of claim 147, wherein said composition comprises a vector.

150. The composition of claim 147, wherein the stringent conditions are
20 high stringency southern hybridization conditions.

151. The composition of claim 147, further comprising a P4 leader sequence (SEQ ID NO. 322).

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152. The composition of claim 147, wherein the polynucleotide is a recombinant polynucleotide.

5 153. The composition of claim 147, wherein the polynucleotide is isolated from a natural source.

154. The composition of claim 147, wherein said composition additionally comprises a nucleic acid sequence encoding for an additional peptide, polypeptide or
10 protein.

155. A composition comprising:

at least one polynucleotide that (a) encodes at least one protein comprising the amino acid sequence of SEQ ID NO:300, x being any amino acid, the region from
15 amino acid position 5 to amino acid position 9 being any of 0 to 5 amino acids, the region from amino acid position 67 to amino acid position 69 being any of 0 to 3 amino acids; and amino acid position 156 being any of 0 to 1 amino acid, or (b) hybridizes under stringent conditions to any of the polynucleotides described in (a).

20 156. The composition of claim 155, additionally comprising a P4 leader sequence (SEQ ID NO. 322).

157. A composition comprising:

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(a) at least one polynucleotide that encodes at least one of: (i) at least one protein comprising the amino acid sequence of any of even numbered SEQ ID NOS:2-252; (ii) at least one protein encoded by a polynucleotide that hybridizes under stringent conditions to a polynucleotide comprising the nucleic acid sequence of any of
5 odd numbered SEQ ID NOS:1-253, (iii) at least one immunogenic portion of at least one protein described in (i) or (ii); or (iv) at least one biological equivalent of at least one protein described in (i) or (ii) or immunogenic fragment described in (iii) or

(b) at least one polynucleotide that hybridizes under stringent conditions to any of the polynucleotides described in (a).

10

158. The composition of claim 157, wherein said at least one polynucleotide comprises the nucleic acid sequence of any of the odd numbered SEQ ID NOS: 1-253.

15 159. The composition of claim 157, wherein said composition comprises a vector.

160. The composition of claim 157, wherein the stringent conditions are high stringency southern hybridization conditions.

20

161. The composition of claim 157, wherein said composition additionally comprises a nucleic acid sequence encoding for an additional peptide, polypeptide or protein.

25 162. A composition comprising:

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(a) at least one polynucleotide that encodes at least one antigen of a first bacterial strain of *Neisseria species* that provides immunogenicity against infection of a subject by a second bacterial strain of *Neisseria species*.; or

5 (b) at least one polynucleotide that hybridizes under stringent conditions to at least one polynucleotide of (a).

163. The composition of claim 162, wherein said at least one isolated polynucleotide comprises the nucleic acid sequence of any of the odd numbered SEQ ID NOS: 1-253.

10

164. The composition of claim 162, additionally comprising a P4 leader sequence (SEQ ID NO. 322).

15

165. The composition of claim 162, wherein said composition comprises a vector.

166. The composition of claim 162, wherein the stringent conditions are high stringency southern hybridization conditions.

20

167. The composition of claim 162, wherein said composition additionally comprises a nucleic acid sequence encoding for an additional peptide, polypeptide or protein.

168. A composition comprising:

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a vector comprising any of:

(a) at least one protein comprising the amino acid sequence of any of SEQ ID NOS:254-259, 260-278 or 279-299; or

5 (b) at least one immunogenic portion of at least one protein described in (a); or

(c) at least one biological equivalent of at least one protein described in (a) or immunogenic fragment described in (b).

10 169. The composition of claim 168, wherein the vector is a plasmid.

170. The composition of claim 168, wherein the vector is a phage.

171. The composition of claim 168, wherein the vector is a bacteriophage.

15 172. The composition of claim 168, wherein the vector is a moderate phage.

173. A composition comprising:

a vector comprising at least one polynucleotide that encodes a protein comprising the amino acid sequence of SEQ ID NO:300;

20 wherein x is any amino acid;

wherein the region from amino acid position 5 to amino acid position 9 is any of 0 to 5 amino acids;

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wherein the region from amino acid position 67 to amino acid position 69 is any of 0 to 3 amino acids; and

wherein amino acid position 156 is any of 0 to 1 amino acid.

5 174. The composition of claim 173, wherein the vector is a plasmid.

175. The composition of claim 173, wherein the vector is a phage.

176. A composition comprising:

10 a vector comprising any of:

(a) at least one polynucleotide that encodes at least one of the polypeptides of the even numbered SEQ ID NOS: 2-252; or

(b) at least one polynucleotide that hybridizes under stringent conditions to at least one polynucleotide of (a).

15

177. The composition of claim 176, wherein the vector comprises the nucleic acid sequence of any of SEQ ID NOS:1-153.

177. The composition of claim 176, wherein the vector is a plasmid.

20

178. The composition of claim 176, wherein the vector is a phage.

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179. The composition of claim 176, wherein the vector is a bacteriophage.

180. The composition of claim 176, wherein the vector is a moderate phage.

5

181. A composition comprising:

a host cell transformed/transfected or infected with a vector, said vector comprising any of:

- 10 (a) at least one protein encoded by an open reading frame of *Neisseria species* (ORF2086), said open reading frame encoding a crossreactive immunogenic antigen, and said crossreactive immunogenic antigen providing immunogenicity against infection by *Neisseria meningitidis* serogroup B in a subject; or
- (b) at least one immunogenic portion of at least one protein described in (a); or
- 15 (c) at least one biological equivalent of at least one protein described in (a) or immunogenic fragment described in (b).

182. A composition comprising:

20 a host cell transformed/transfected or infected with a vector, said vector comprising any of :

- (a) at least one protein comprising any of SEQ ID NOS:254-259, 260-278 or 279-299; or

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(b) at least one immunogenic portion of at least one protein described in (a); or

(c) at least one biological equivalent of at least one protein described in (a) or immunogenic fragment described in (b).

5

183. A composition prepared by a process comprising:

expressing in a host cell a nucleic acid sequence encoding any of:

(a) at least one protein encoded by an open reading frame of *Neisseria species* (ORF2086), said open reading frame encoding a crossreactive immunogenic antigen, and said crossreactive immunogenic antigen providing immunogenicity against infection by *Neisseria meningitidis* serogroup B in a subject; or

(b) at least one immunogenic portion of at least one protein described in (a); or

(c) at least one biological equivalent of at least one protein described in (a) or immunogenic fragment described in (b).

15

184. The composition of claim 183, wherein the nucleic acid sequence is any of the odd numbered SEQ ID NOS: 1-253.

20 185. The composition of claim 183, wherein the nucleic acid sequence encodes a protein comprising any of the even numbered SEQ ID NOS: 2-252.

186. The composition of claim 183, wherein the nucleic acid sequence encodes a protein comprising any of even numbered SEQ ID NOS: 2-174.

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187. The composition of claim 183, wherein the protein has a molecular weight of about 26,000 to about 30,000 as measured by mass spectroscopy.

5 188. The composition of claim 187, wherein the protein has a molecular weight of about 28-35 kDa as measured on a 10%-20% SDS polyacrylamide gel.

189. The composition of claim 183, wherein said composition additionally comprises a pharmaceutically acceptable buffer, diluent, adjuvant or carrier.

10

190. The composition of claim 183, wherein said composition additionally comprises a carrier.

15 191. The composition of claim 183, wherein said composition additionally comprises an adjuvant.

192. The composition of claim 191, wherein the adjuvant is a liquid.

20 193. The composition of claim 183, wherein the protein is a lipidated protein.

194. A composition prepared by a process comprising:

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isolating and purifying from *Neisseria species* any of:

- 5 (a) at least one protein encoded by an open reading frame of *Neisseria species* (ORF2086), said open reading frame encoding a crossreactive immunogenic antigen, and said crossreactive immunogenic antigen providing immunogenicity against infection by *Neisseria meningitidis* serogroup B in a subject; or
- (b) at least one immunogenic portion of at least one protein described in (a); or
- (c) at least one biological equivalent of at least one protein described in (a) or immunogenic fragment described in (b).

10

195. The composition of claim 194, wherein the at least one polynucleotide comprises the nucleic acid sequence of any of the odd numbered SEQ ID NOS: 1-253.

- 15 196. The composition of claim 194, wherein the process further comprises introducing a non-native leader sequence to the at least one isolated polynucleotide.

197. The composition of claim 196, wherein the non-native leader sequence is P4 leader sequence (SEQ ID NO. 322).

20

198. A composition prepared by a process comprising:

isolating and purifying from *Neisseria species* any of:

- (a) at least one protein comprising any of SEQ ID NOS:254-259, 260-278 or 279-299; or

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(b) at least one immunogenic portion of at least one protein described in (a); or

(c) at least one biological equivalent of at least one protein described in (a) or immunogenic fragment described in (b)..

5

199. The composition of claim 198, wherein the polypeptide has a molecular weight of about 26,000 to about 30,000 as measured by mass spectroscopy.

10 200. The composition of claim 199, wherein the polypeptide has a molecular weight of about 28-35 kDa as measured on a 10%-20% SDS polyacrylamide gel.

201. The composition of claim 198, wherein said composition additionally comprises a pharmaceutically acceptable buffer, diluent, adjuvant or carrier.

15

202. The composition of claim 198, wherein said composition additionally comprises a carrier.

20 203. The composition of claim 198, wherein said composition additionally comprises an adjuvant.

204. The composition of claim 203, wherein said adjuvant comprises a liquid.

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205. The composition of claim 198, wherein the protein is a lipidated protein.

5 206. A composition prepared by a process comprising:

inserting into a vector at least one isolated protein comprising the amino acid sequence of SEQ ID NO:300;

wherein x is any amino acid;

10 wherein the region from amino acid position 5 to amino acid position 9 is any of 0 to 5 amino acids;

wherein the region from amino acid position 67 to amino acid position 69 is any of 0 to 3 amino acids; and

wherein amino acid position 156 is any of 0 to 1 amino acid.

15 207. The composition of claim 206, wherein the vector is a plasmid.

208. The composition of claim 206, wherein the vector is a phage.

209. The composition of claim 206, wherein the vector is a bacteriophage.

20

210. The composition of claim 206, wherein the vector is a moderate phage.

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211. The composition of claim 206, further comprising a non-native leader sequence

5 212. The composition of claim 211, wherein the non-native leader sequence is P4 leader sequence (SEQ ID NO. 322).

213. A composition prepared by a process comprising:

10 expressing in a host cell (a) at least one isolated polynucleotide that encodes at least one protein encoded by an open reading frame of *Neisseria species* (ORF2086) or at least one immunogenic portion or biological equivalent of said at least one protein, said open reading frame encoding a crossreactive immunogenic antigen, and said crossreactive immunogenic antigen providing immunogenicity against infection by *Neisseria meningitidis* serogroup B in a subject, and (b) a non-native leader
15 sequence associated with said at least one isolated polynucleotide.

214. The composition of claim 213, wherein the non-native leader sequence is P4 leader sequence (SEQ ID NO. 322).

20 215. A composition prepared by a process comprising:

 expressing in a host cell a nucleic acid sequence encoding any of:

 (a) at least one protein encoded by an open reading frame of *Neisseria species* (ORF2086), said open reading frame encoding a crossreactive immunogenic

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antigen, and said crossreactive immunogenic antigen providing immunogenicity against infection by *Neisseria meningitidis* serogroup B in a subject; or

(b) at least one immunogenic portion of at least one protein described in (a); or

5 (c) at least one biological equivalent of at least one protein described in (a) or immunogenic fragment described in (b); or

expressing in a host cell a nucleic acid sequence that hybridizes under stringent conditions to the foregoing nucleic acid sequence.

10 216. The composition of claim 215, wherein the nucleic acid sequence is any of the odd numbered SEQ ID NOS: 1-253;

217. The composition of claim 215, wherein the nucleic acid sequence encodes any of the even numbered SEQ ID NOS: 2-252.

15

218. The composition of claim 215, wherein the protein has a molecular weight of about 26,000 to about 30,000 as measured by mass spectroscopy.

219. The composition of claim 218, wherein the protein has a molecular
20 weight of about 28-35 kDa as measured on a 10%-20% SDS polyacrylamide gel.

220. The composition of claim 215, wherein said composition additionally comprises a pharmaceutically acceptable buffer, diluent, adjuvant or carrier.

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221. The composition of claim 215, wherein said composition additionally comprises a carrier.

5 222. The composition of claim 215, wherein said composition additionally comprises an adjuvant.

223. The composition of claim 222, wherein said adjuvant comprises a liquid.

10

224. The composition of claim 215, wherein the stringent conditions are high stringency southern hybridization conditions.

225. A composition prepared by a process comprising:

15 isolating and purifying from *Neisseria species* any of:

(a) at least one polynucleotide that encodes at least one of the polypeptides comprising the amino acid sequence of any of the even numbered SEQ ID NOS: 2-252; or

(b) at least one polynucleotide that hybridizes under stringent conditions to
20 at least one polynucleotide of (a).

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226. The composition of claim 225, wherein the at least one polynucleotide comprises the nucleic acid sequence of any of the odd numbered SEQ ID NOS: 1-253.

5 227. The composition of claim 225, wherein the process further comprises introducing a non-native leader sequence to the at least one polynucleotide.

228. The composition of claim 227, wherein the non-native leader sequence is P4 leader sequence (SEQ ID NO. 322).

10

229. A composition prepared by a process comprising:

isolating and purifying from *Neisseria species* any of:

(a) at least one protein comprising the amino acid sequence of any of even numbered SEQ ID NOS:2-252;

15 (b) at least one protein encoded by a polynucleotide that hybridizes under stringent conditions to a polynucleotide comprising the nucleic acid sequence of any of odd numbered SEQ ID NOS:1-253;

(c) at least one immunogenic portion of at least one protein described in (a) or (b); or

20 (d) at least one biological equivalent of at least one protein described in (a) or (b) or immunogenic fragment described in (c).

230. The composition of claim 229, wherein the protein has a molecular weight of about 26,000 to about 30,000 as measured by mass spectroscopy.

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231. The composition of claim 230, wherein the protein has a molecular weight of about 28-35 kDa as measured on a 10%-20% SDS polyacrylamide gel.

5 232. The composition of claim 229, wherein said composition additionally comprises a pharmaceutically acceptable buffer, diluent, adjuvant or carrier.

233. The composition of claim 229, wherein said composition additionally comprises a carrier.

10

234. The composition of claim 229, wherein said composition additionally comprises an adjuvant.

15 235. The composition of claim 234, wherein said adjuvant comprises a liquid.

236. The composition of claim 229, wherein the stringent conditions are high stringency southern hybridization conditions.

20 237. A composition prepared by a process comprising:

inserting into a vector any of:

(a) at least one isolated polynucleotide that encodes at least one polypeptides comprising any of the even numbered SEQ ID NOS: 2-252; or

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(b) at least one isolated polynucleotide that hybridizes under stringent conditions to at least one polynucleotide of (a).

238. The composition of claim 237, wherein the vector is a plasmid.

5

239. The composition of claim 237, wherein the vector is a phage.

240. The composition of claim 237, wherein the vector is a bacteriophage.

10

241. The composition of claim 237, wherein the vector is a moderate phage.

242. The composition of claim 237, further comprising a non-native leader sequence

15

243. The composition of claim 242, wherein the non-native leader sequence is P4 leader sequence (SEQ ID NO. 322).

244. A composition prepared by a process comprising:

20 expressing in a host cell at least one polynucleotide that (a) encodes at least one protein encoded by an open reading frame of *Neisseria species* (ORF2086) or at least one immunogenic portion or biological equivalent of said at least one protein, said open reading frame encoding a crossreactive immunogenic antigen, and said crossreactive immunogenic antigen providing immunogenicity against infection by

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Neisseria meningitidis serogroup B in a subject; or (b) hybridizes under stringent conditions to any of the polynucleotides described in (a).

245. The composition of claim 244, additionally comprising a non-native
5 leader sequence associated with said at least one polynucleotide.

246. The composition of claim 245, wherein the non-native leader sequence is P4 leader sequence (SEQ ID NO. 322).

10 247. A composition comprising:

at least one immunogenic non-strain specific *Neisseria meningitidis* antigen, said antigen being nonpathogenic and substantially free from any infectious impurities.

15 248. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:2-6.

20 249. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:8-12.

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250. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:14-18.

5 251. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:20-24.

10 252. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:26-30.

253. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:32-36.

15

254. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:38-42.

20 255. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:44-48.

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256. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:50-54.

5 257. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:56-60.

10 258. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:62-66.

15 259. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:68-72.

20 260. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:74-78.

 261. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:80-84.

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262. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:86-90.

5 263. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:92-96.

10 264. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:98-102.

15 265. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:104-108.

20 266. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:110-114.

267. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:116-120.

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268. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:122-126.

5 269. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:128-132.

10 270. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:134-138.

15 271. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:140-144.

20 272. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:146-150.

273. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:152-156.

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274. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:158-162.

5 275. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:164-168.

10 276. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:170-174.

15 277. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:176-180.

20 278. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:182-186.

279. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:188-192.

-174-

280. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:194-198.

5 281. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:200-204.

10 282. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:206-210.

15 283. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:212-216.

20 284. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:218-222.

285. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:224-228.

-175-

286. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:230-234.

5 287. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:236-240.

10 288. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:242-246.

15 289. The antigen of claim 247, wherein the antigen comprises an amino acid sequence having at least about 70% amino acid sequence identity to any of even numbered SEQ ID NOS:248-252.

290. Use of the composition of any of claims 1-289 in the preparation of a medicament for inducing an immune response in a mammal.

20 291. The use according to claim 290, wherein said composition is administered parenterally.

292. The use according to claim 290, wherein said composition is administered mucosally.

-176-

293. The use of the composition of any of claims 1-289 in a medicament effective against bacterial meningitis in a mammal.

5 294. The use of the composition according to claim 293, wherein said composition is administered parenterally.

295. The use of the composition according to claim 293, wherein said composition is administered mucosally.

10

296. The use of the composition according to claim 293, wherein the composition is administered by subcutaneous or intramuscular injection.

297. A method of preparing a composition comprising:

15 expressing in a host cell a nucleic acid sequence encoding any of:

(a) at least one protein encoded by an open reading frame of *Neisseria species* (ORF2086), said open reading frame encoding a crossreactive immunogenic antigen, and said crossreactive immunogenic antigen providing immunogenicity against infection by *Neisseria meningitidis* serogroup B in a subject; or

20 (b) at least one immunogenic portion of at least one protein described in (a); or

(c) at least one biological equivalent of at least one protein described in (a) or immunogenic fragment described in (b).

-177-

298. The method of claim 297, wherein the nucleic acid sequence is expressed *in vivo*.

5 299. The method of claim 297, wherein the nucleic acid sequence is expressed *in vitro*.

300. The method of claim 297, further comprising associating a P4 leader sequence (SEQ ID NO. 322).

10 301. The method of claim 297, wherein the at least one protein comprises any of the SEQ ID NOS: 254-299.

302. A method of preparing a composition comprising:

isolating and purifying from *N. meningitidis* at least one polynucleotide that
15 (a) encodes at least one protein encoded by an open reading frame of *Neisseria species* (ORF2086) or at least one immunogenic portion or biological equivalent of said at least one protein, said open reading frame encoding a crossreactive immunogenic antigen, and said crossreactive immunogenic antigen providing immunogenicity against infection by *Neisseria meningitidis* serogroup B in a subject;
20 or (b) hybridizes under stringent conditions to any of the polynucleotides described in (a).

303. The method of claim 302, wherein the stringent conditions are high stringency southern hybridization conditions.

304. A method of preparing a composition comprising:

isolating and purifying from *Neisseria species* any of the proteins, immunogenic portions or biological equivalents described herein.

5

305. A method of preparing an antibody composition comprising:

recovering antibodies from an animal after introducing into the animal a composition comprising any of the proteins, immunogenic portions or biological equivalents described herein.

10

306. A method of inducing an immune response in a mammal comprising:

administering to the mammal an effective amount of one or more of the compositions of claims 1-289.

15

307. The method of claim 306, wherein said composition is administered parenterally.

308. The method of claim 306, wherein said composition is administered mucosally.

20

309. A method of preventing or treating bacterial meningitis in a mammal comprising:

-179-

administering to the mammal an effective amount of one or more of the compositions of claims 1-289.

310. The method of claim 309, wherein said composition is administered
5 parenterally.

311. The method of claim 309, wherein said composition is administered
mucosally.

10 312. The method of claim 309, wherein the composition is administered by subcutaneous or intramuscular injection.

313. A method of preventing or treating bacterial meningitis in a mammal comprising:

15 administering to the mammal an effective amount of an antibody composition comprising antibodies that immunospecifically bind with a protein, immunogenic portion or biological equivalent comprising the amino acid sequence of any of the even numbered SEQ ID NOS: 2-252 or any of the SEQ ID NOS: 254-299.

20 313. The method of claim 312, wherein the antibody composition is administered parenterally.

314. The method of claim 312, wherein the antibody composition is administered mucosally.

315. The method of claim 312, wherein the antibody composition is administered by subcutaneous or intramuscular injection.

5 316. A method of preparing a composition comprising:

expressing in a host cell a nucleic acid sequence encoding any of:

(a) at least one protein comprising the amino acid sequence of any of even numbered SEQ ID NOS:2-252 or any of the SEQ ID NOS: 254-299;

10 (b) at least one protein encoded by a polynucleotide that hybridizes under stringent conditions to a polynucleotide comprising the nucleic acid sequence of any of odd numbered SEQ ID NOS:1-253;

(c) at least one immunogenic portion of at least one protein described in (a) or (b); or

15 (d) at least one biological equivalent of at least one protein described in (a) or (b) or immunogenic fragment described in (c).

317. The method of claim 316, wherein the nucleic acid sequence is expressed *in vivo*.

20 318. The method of claim 316, wherein the nucleic acid sequence is expressed *in vitro*.

319. The method of claim 316, wherein the vector is a plasmid.

-181-

320. The method of claim 316, wherein the vector is a phage.

321. The method of claim 316, further comprising associating a non-native
5 leader sequence with said at least one isolated polynucleotide.

322. The method of claim 316, wherein the non-native leader sequence is
P4 leader sequence (SEQ ID NO. 267).

10 323. A method of preparing a composition comprising:

isolating and purifying from *Neisseria species* at least one isolated protein
comprising the amino acid sequence of SEQ ID NO:300;

wherein x is any amino acid;

wherein the region from amino acid position 5 to amino acid position 9 is any
15 of 0 to 5 amino acids;

wherein the region from amino acid position 67 to amino acid position 69 is
any of 0 to 3 amino acids; and

wherein amino acid position 156 is any of 0 to 1 amino acid.

20 324. The method of claim 323, further comprising introducing a non-native
leader sequence to the at least one isolated polynucleotide.

-182-

325. The method of claim 323, wherein the non-native leader sequence is P4 leader sequence (SEQ ID NO. 322).

326. A method of preparing a composition comprising:

5 isolating and purifying from *Neisseria species* any of:

(a) at least one protein comprising the amino acid sequence of any of the even numbered SEQ ID NOS: 2-252 or the amino acid sequence of any of SEQ ID NOS:254-259, 260-278 or 279-299; or

10 (b) at least one protein encoded by a polynucleotide that hybridizes under stringent conditions to a polynucleotide comprising the nucleic acid sequence of any of the odd numbered SEQ ID NOS: 1-253.

327. The method of claim 326, wherein the stringent conditions are high stringency southern hybridization conditions.

15

328. A method of preparing an antibody composition comprising:

recovering antibodies from an animal after introducing into the animal a composition comprising:

20 (a) at least one protein comprising the amino acid sequence of any of the even numbered SEQ ID NOS: 2-252 or the amino acid sequence of any of SEQ ID NOS:254-259, 260-278 or 279-299; or

(b) at least one protein encoded by a polynucleotide that hybridizes under stringent conditions to the polynucleotide of any of the odd numbered SEQ ID NOS: 1-253.

-183-

329. The method of claim 328, wherein the stringent conditions are high stringency southern hybridization conditions.

5 330. A transformed/transfected or infected cell line comprising:

a recombinant cell that expresses a nucleic acid sequence that (a) encodes at least one isolated protein comprising the amino acid sequence of any of SEQ ID NOS:254-259, 260-278 or 279-299, or (b) hybridizes under stringent conditions to any of the polynucleotides described in (a).

10

331. A transformed/transfected or infected cell line comprising:

a recombinant cell that expresses a nucleic acid sequence that (a) encodes at least one protein encoded by an open reading frame of *Neisseria species* (ORF2086) or at least one immunogenic portion or biological equivalent of said at least one
15 protein, said open reading frame encoding a crossreactive immunogenic antigen, and said crossreactive immunogenic antigen providing immunogenicity against infection by *Neisseria meningitidis* serogroup B in a subject or (b) hybridizes under stringent conditions to any of the polynucleotides of (a); or

a recombinant cell that expresses a nucleic acid sequence encoding: (c) at least
20 one polypeptide encoded by any of (a) or (b); or (d) at least one polypeptide comprising the amino acid sequence of any of the even numbered SEQ ID NOS: 2-252.

332. The transformed/transfected or infected cell line of claim 331, wherein
25 the polypeptide is a monoclonal antibody.

333. The transformed/transfected or infected cell line of claim 331, wherein the recombinant cell is a hybridoma.

5 334. The transformed/transfected or infected cell line of claim 331, wherein the recombinant cell is a trioma.

335. A transformed/transfected or infected cell line comprising:
a recombinant cell that expresses a nucleic acid sequence comprising:

10 (a) at least one polynucleotide that encodes a protein comprising any of the even numbered SEQ ID NOS: 2-252;

(b) at least one polynucleotide comprising the nucleic acid sequence of any of the odd numbered SEQ ID NOS: 1-253;

15 (c) at least one polynucleotide that hybridizes under stringent conditions to any of (a) or (b); or

a recombinant cell that expresses a nucleic acid sequence encoding:

(d) at least one polypeptide encoded by any of (a), (b) or (c); or

(e) at least one polypeptide comprising the amino acid sequence of any of the even numbered SEQ ID NOS: 2-252.

20

336. The transformed/transfected or infected cell line of claim 335, wherein the polypeptide is a monoclonal antibody.

-185-

337. The transformed/transfected or infected cell line of claim 335, wherein the recombinant cell is a hybridoma.

5 338. The transformed/transfected or infected cell line of claim 335, wherein the recombinant cell is a trioma.

339. A method for identifying an immunogenic protein comprising:
detecting bactericidal activity in a sample tested against an ORF2086 antisera.

10 340. A method for identifying an immunogenic protein comprising:
detecting a polynucleotide in a sample tested against an ORF2086 nucleic acid probe.

341. A composition as substantially hereinbefore described.

15

342. A use substantially as hereinbefore described.

FIG. 1A
Identification of Components in the Unadsorbed TMAE Fraction: SDS-PAGE Isolation of Peptides
(CNBr Cleavage of Unadsorbed TMAE Fraction followed by SDS-PAGE and N-term sequencing of fragments from PVDF blot)



FIG. 1B

Identification of Components in the Unadsorbed TMAE Fraction: Reverse Phase Isolation of Peptides

Enzymatic digestion of unadsorbed TMAE fraction followed by reverse phase chromatography separation of peptides and direct N-terminal sequencing

Enzymatic Digest	Retention Time of Peptide (min)	Molecular Weight of Peptide (d)	N-term. ID
GluC (V8)	6.716	2069.7	P5163
LysC	13.800	3351.2	P4431
LysC	13.800	3351.2	P2086
ArgC	6.860	2278.9	P5163

P4431 (SEQ ID NO: 327)
predicted mw 36,775

P2086 (SEQ ID NO: 212)
predicted mw 27,100

P5163 (SEQ ID NO: 328)
predicted mw 7,081

FIG. 2
Purification of rLP2086

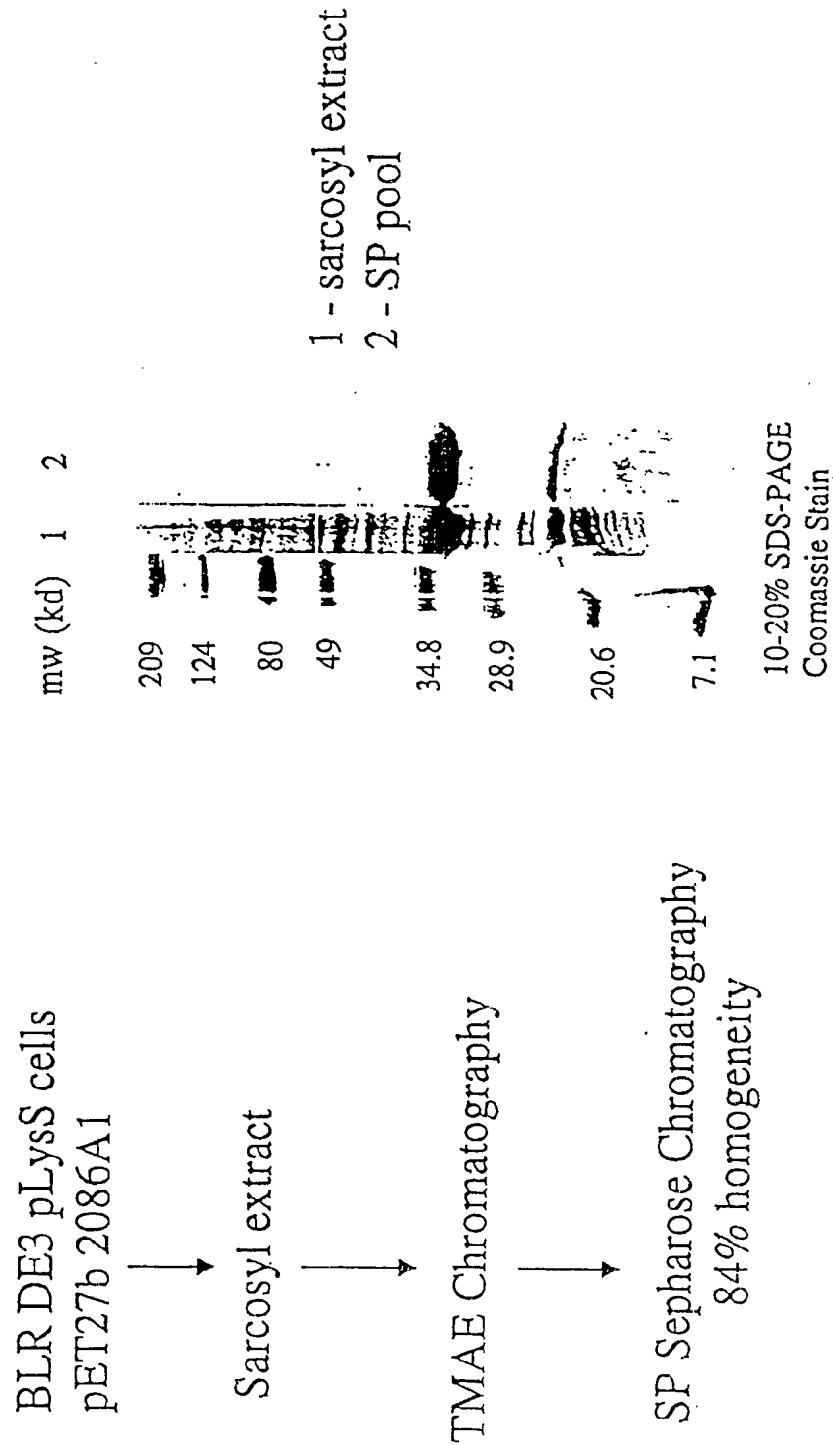


FIG. 3
Identification of Components in the Unadsorbed
TMAE Fraction: LC-MS/MS

SDS-PAGE followed by gel excision, proteolytic digestion, and LC-
MS/MS analysis (Liquid Chromatography tandem Mass Spectrometry)



FIG. 4
Expression of rLP2086

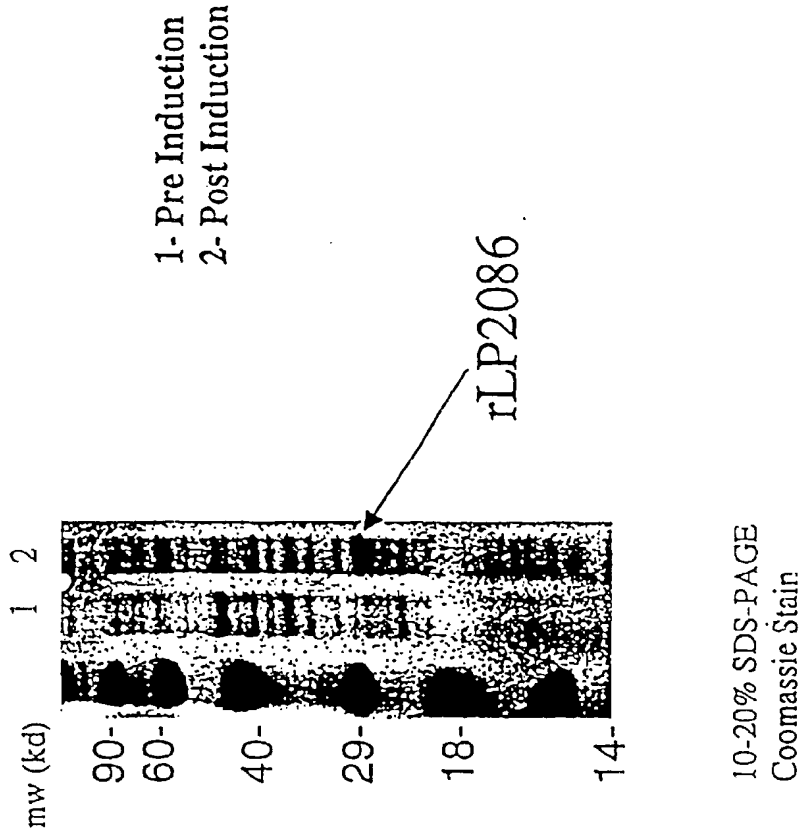


FIG. 5

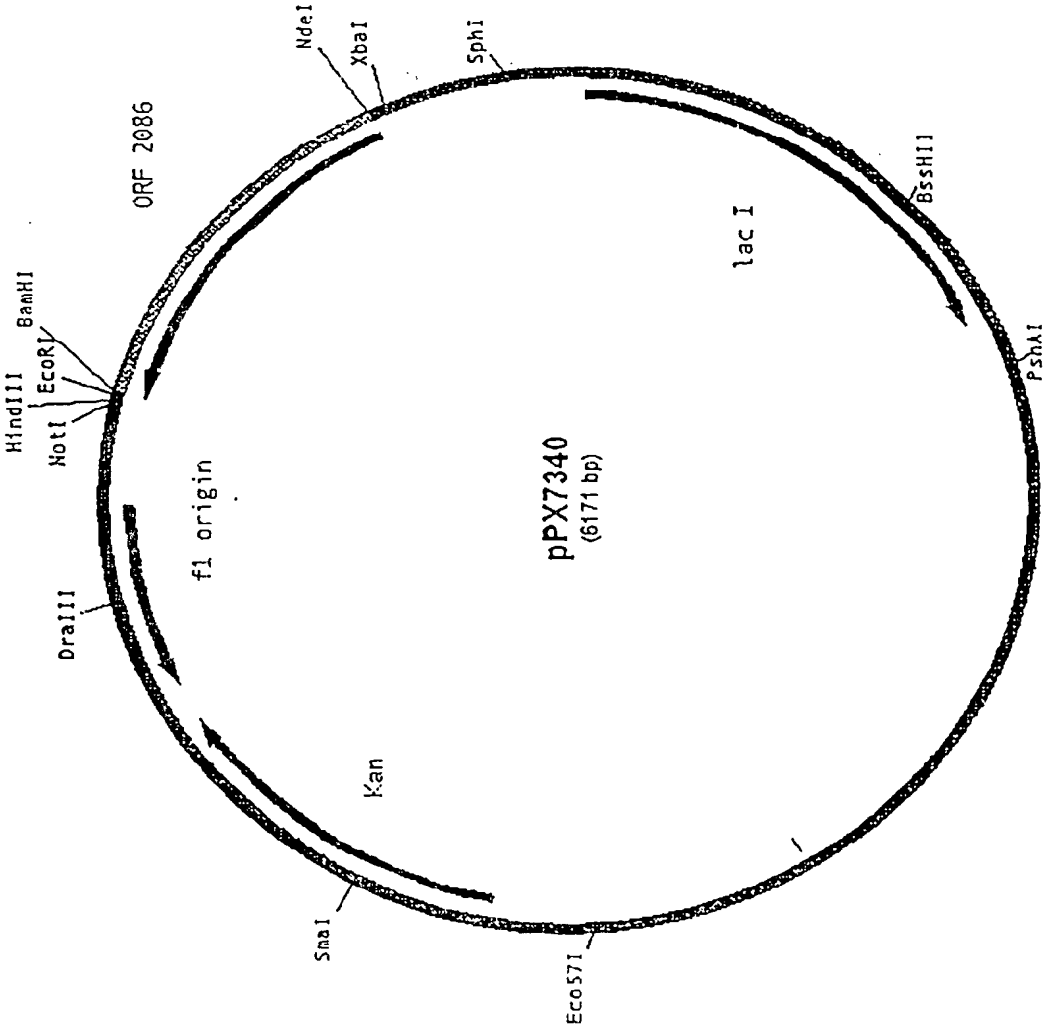


FIG. 6

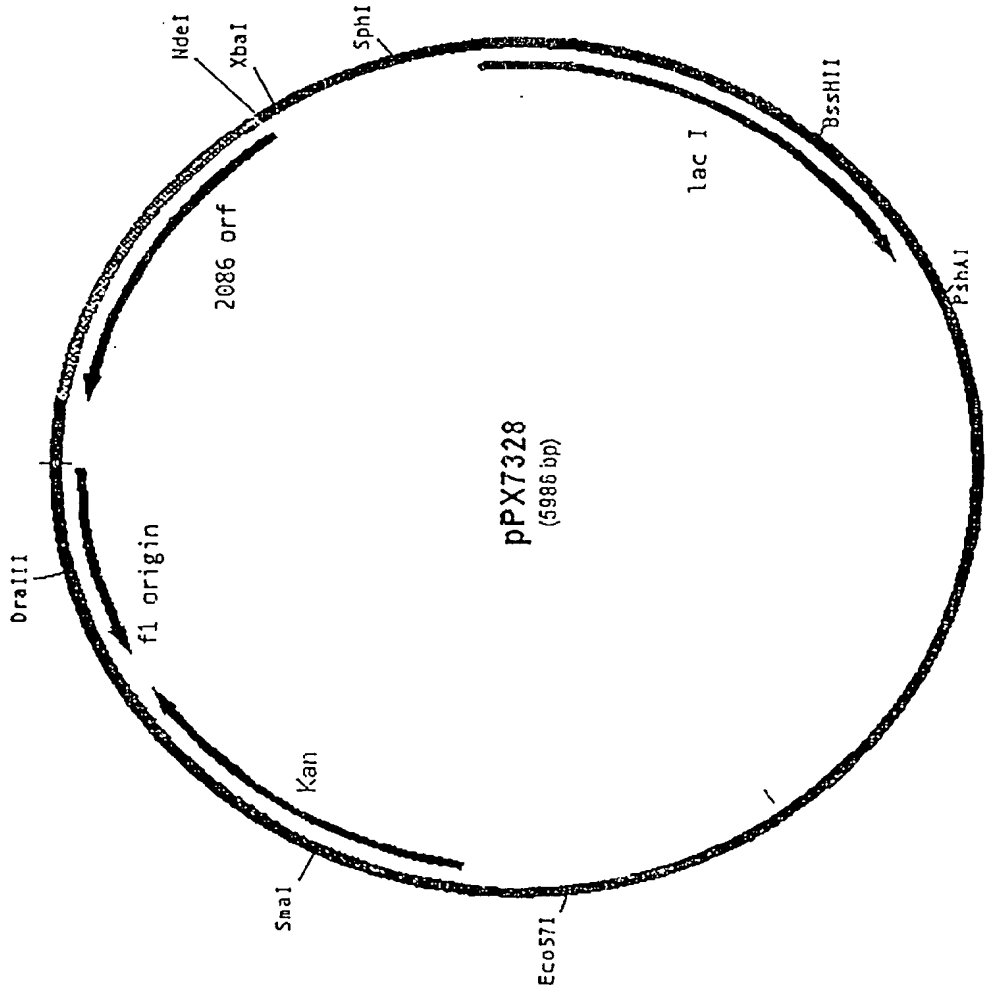


FIG. 7

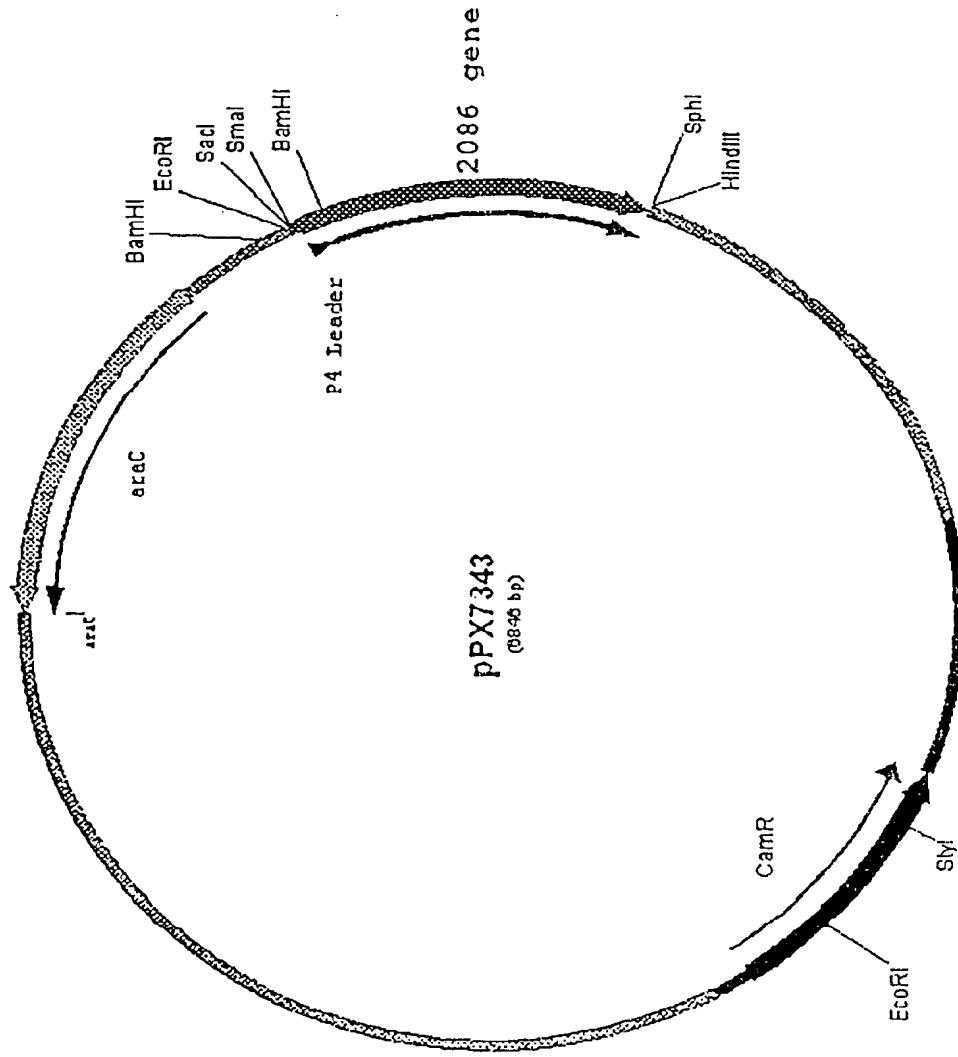


FIG. 8

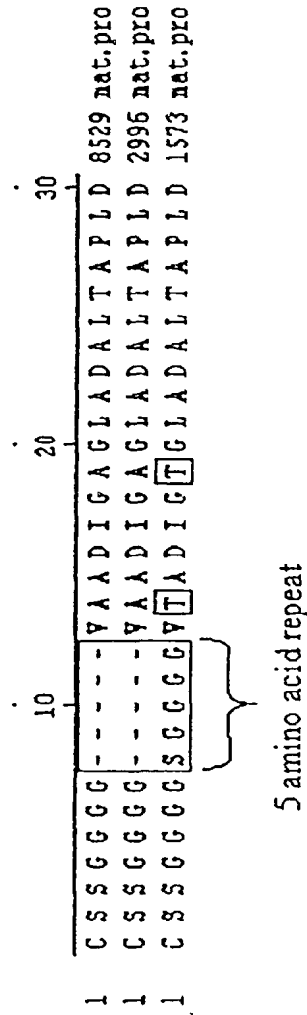


FIG. 9A

Identification of Immunogenic Component in Nm strain 8529

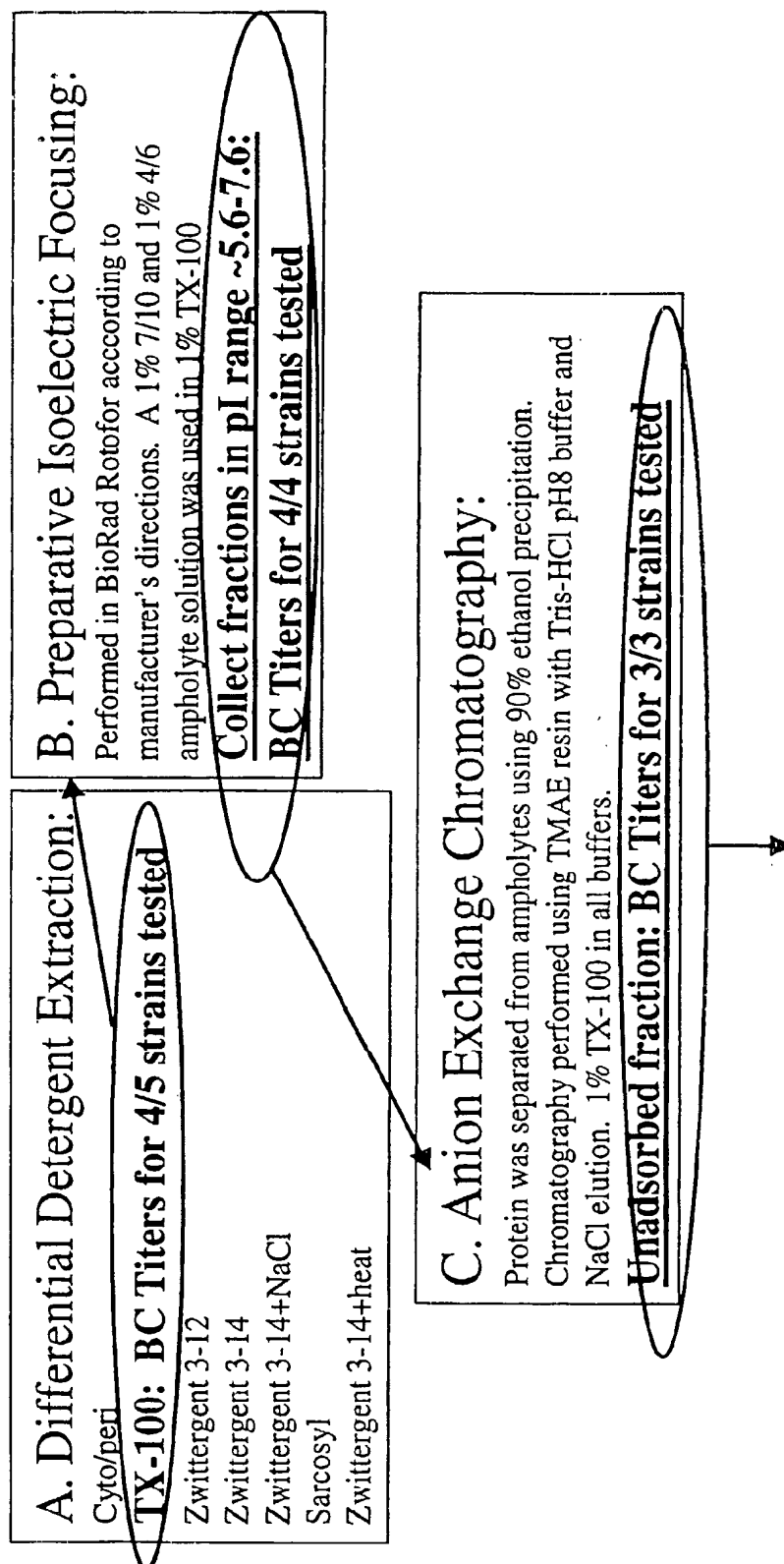
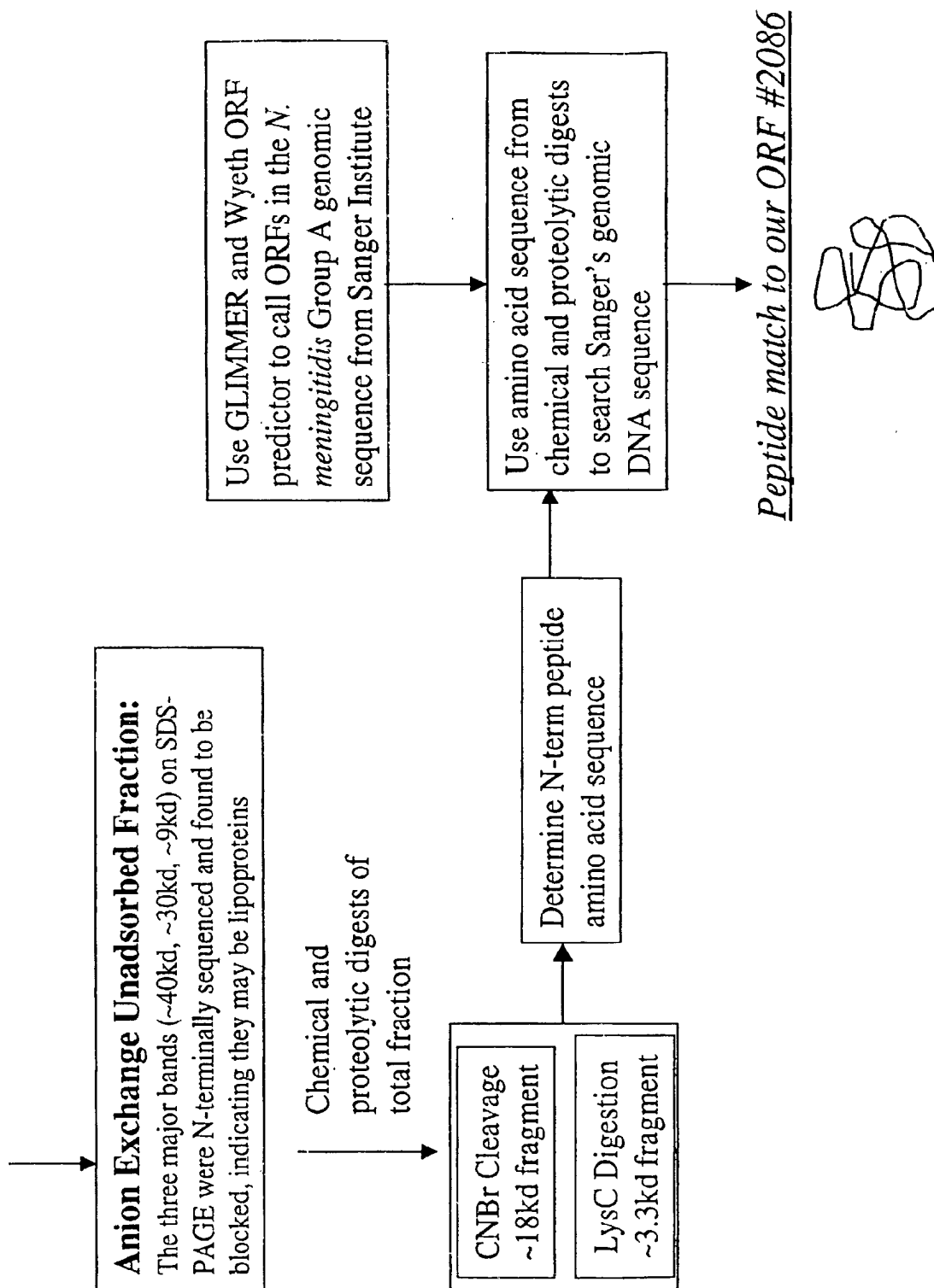


FIG. 9B



Lipidated rP2086
pBAD18-Arabinose promoter

Non-Lipidated rP2086
pET9a-T7 promoter
8529, CDC-1573 and 2996

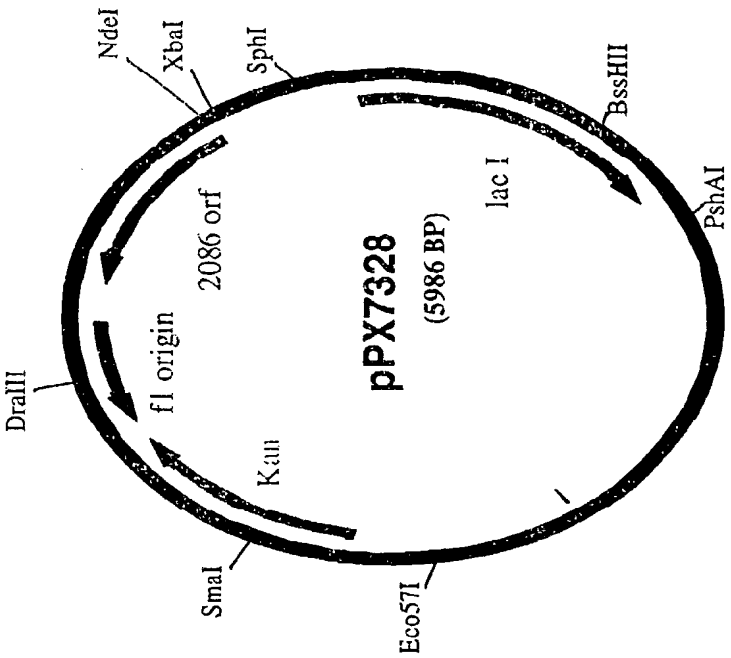


FIG. 10B

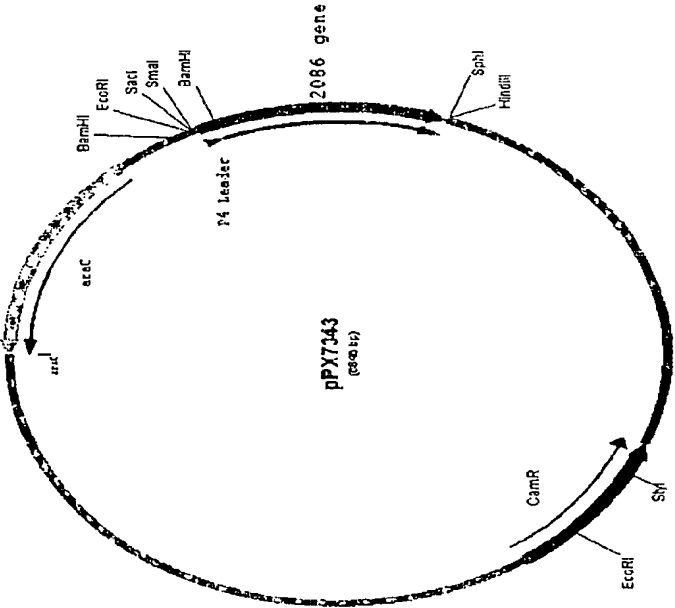
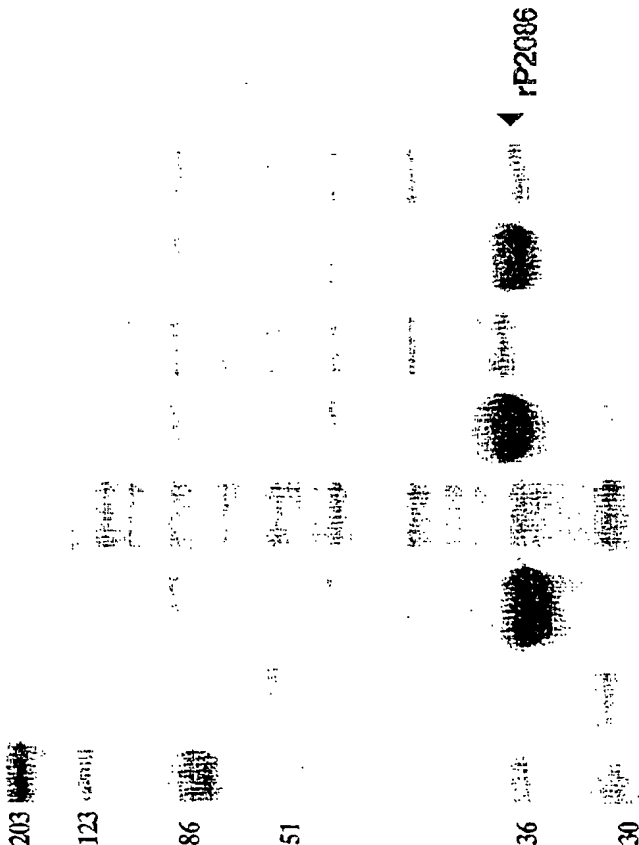


FIG. 10A

rP2086 Expressed in pET/BL21(DE3), IPTG Induction With / Out the T7-Tag

IPTG IPTG IPTG IPTG IPTG
Marker 7328 T7-7328 7328 T7-7334 7334 T7-7344 7344

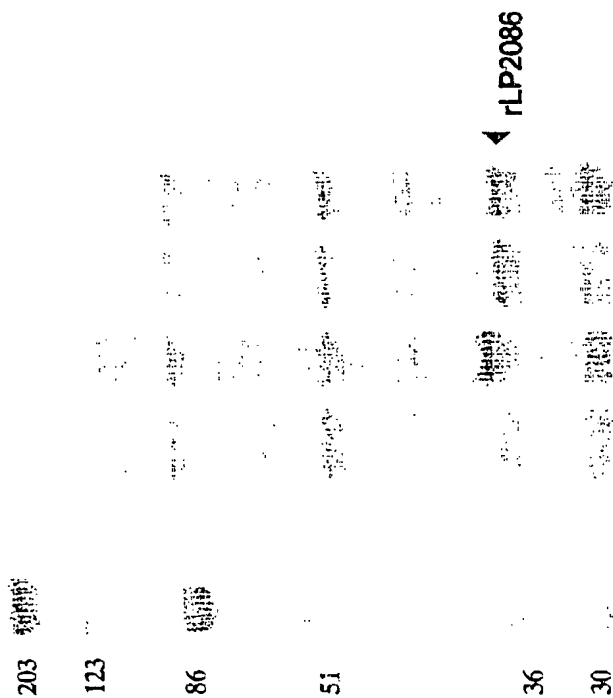


8529 CDC-1573 2996

FIG. 11B

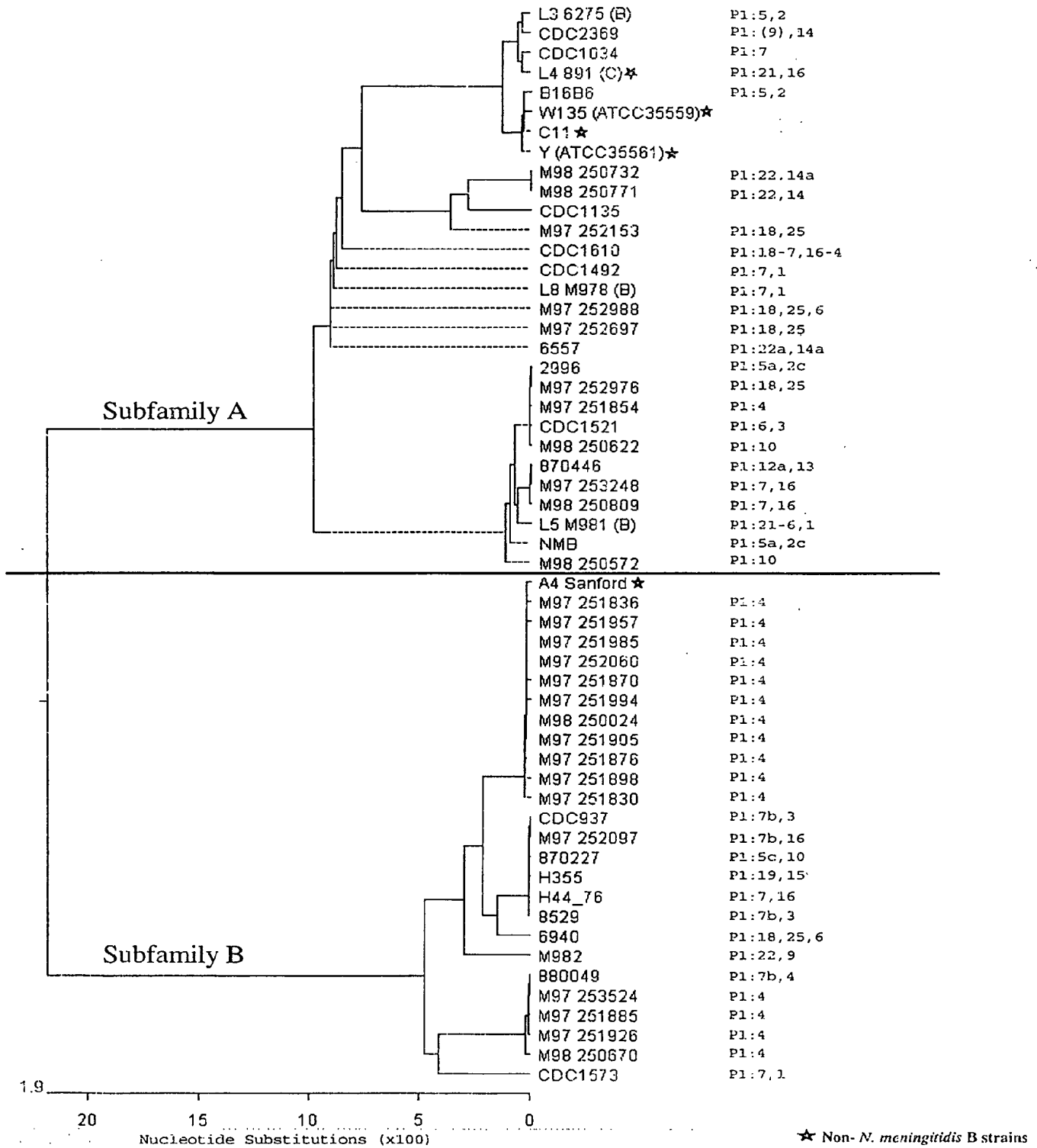
rLP2086 Expressed in pBAD/BLR, Arabinose Induction

Arab. Arab. Arab. Arab.
Marker 7343 PW62 PW105 PW102



8529 1573 2996 250771

FIG. 11A



Whole Cell ELISA Data for rLP2086 Subfamily A Antisera

WO 03/063766

15/20

PCT/US02/32369

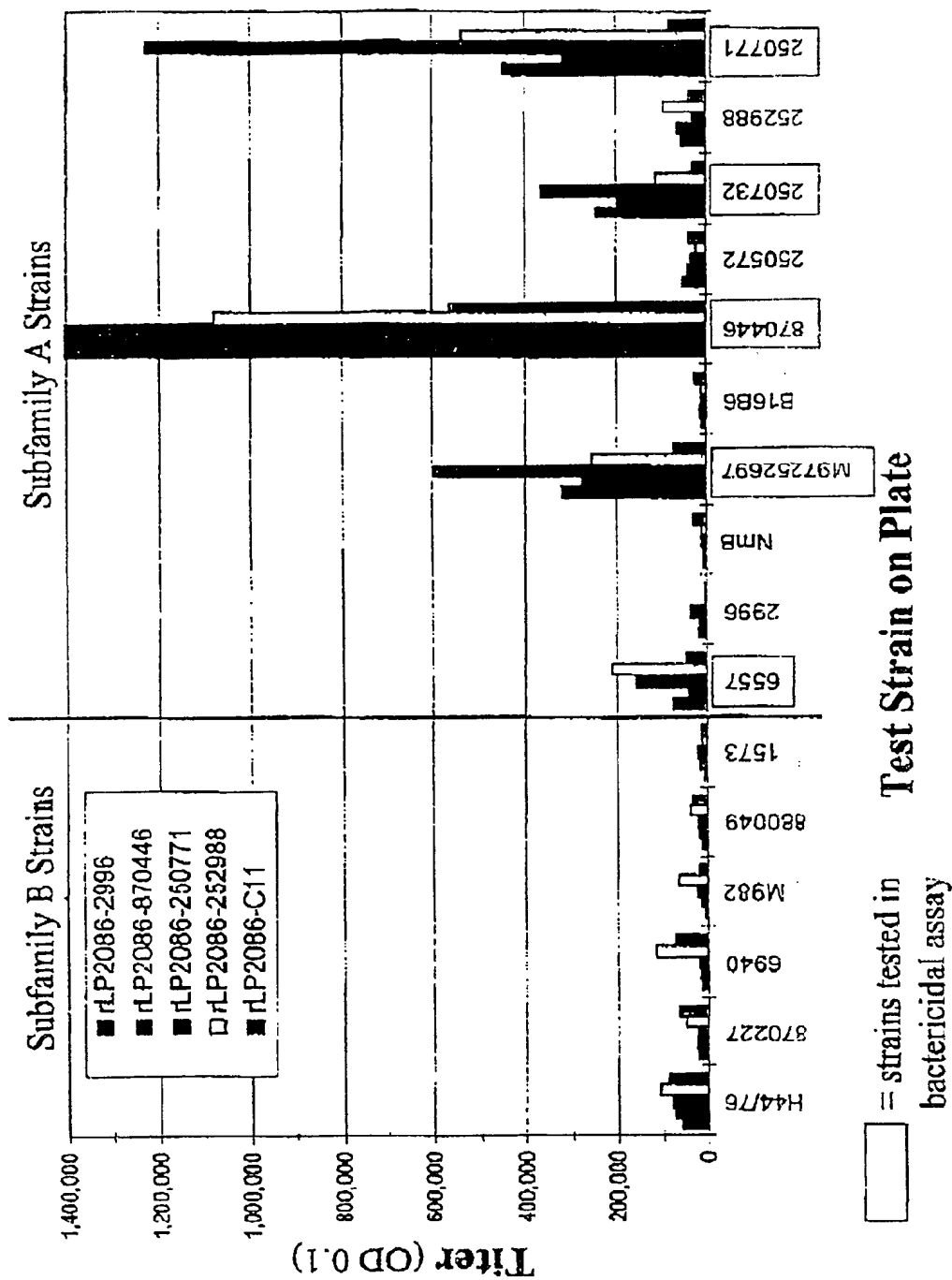


FIG. 13

Whole Cell ELISA Data for rLP2086 Subfamily B Antisera

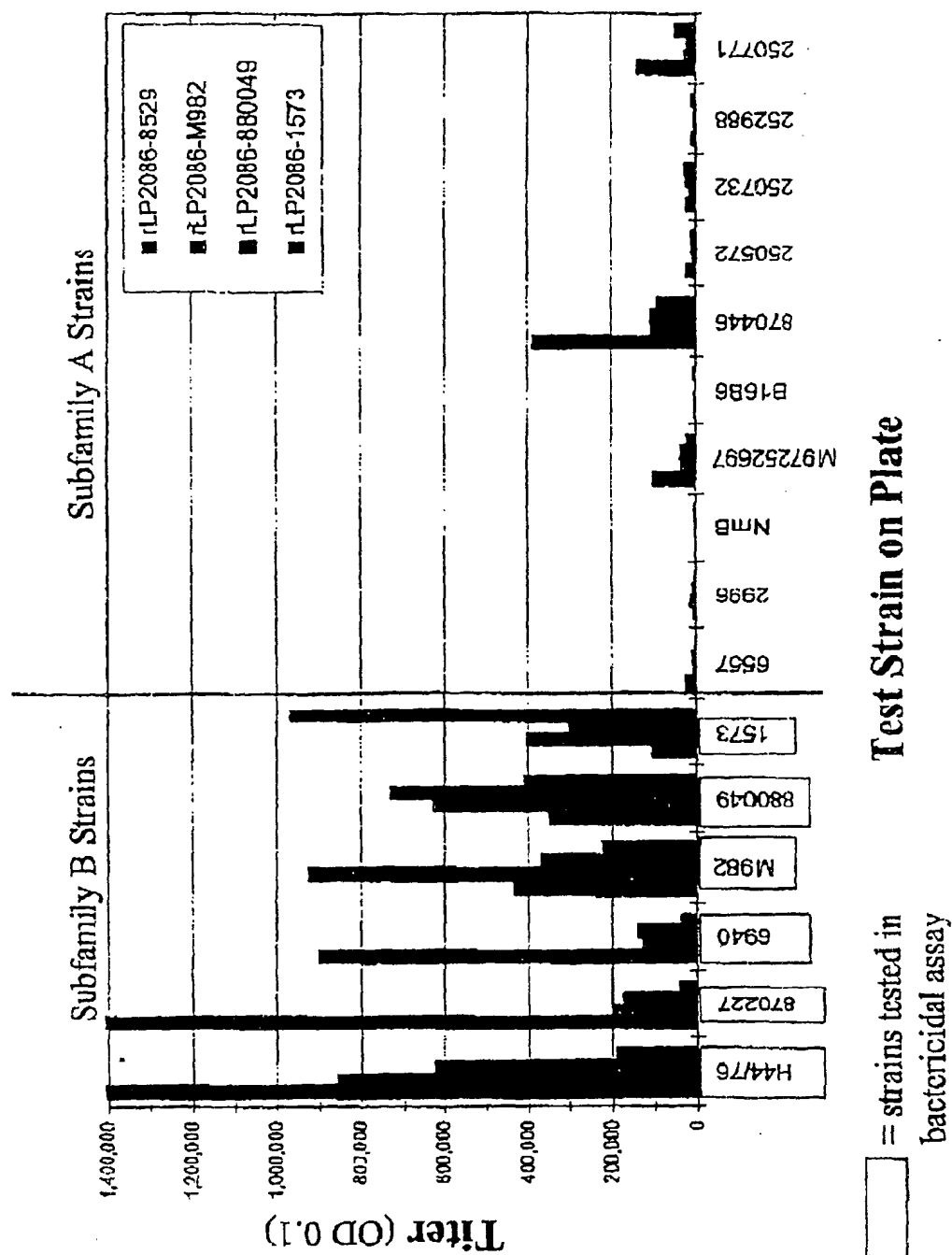


FIG. 14

rLP2086 Mixing Study – WCE Titers

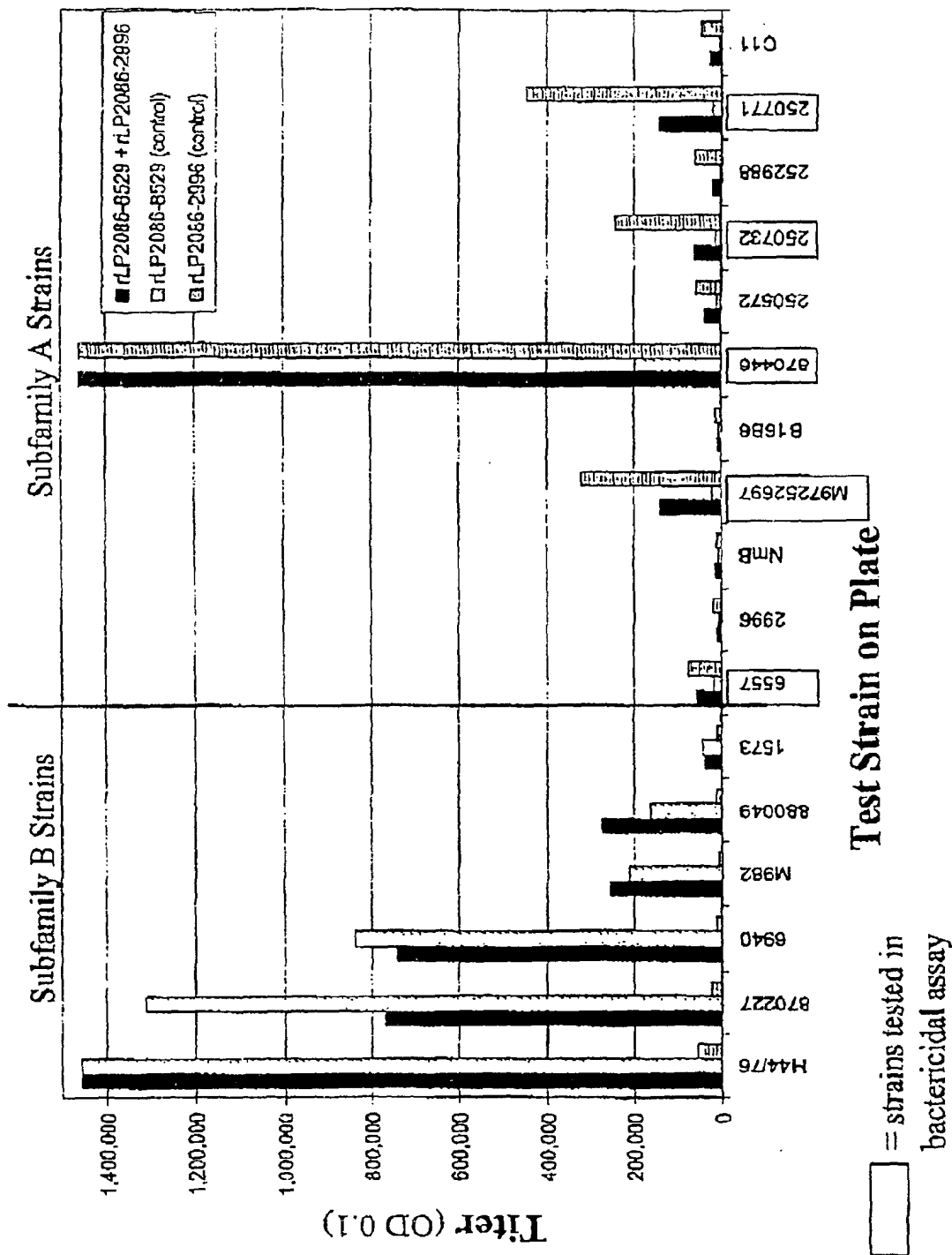


FIG. 15

rLP2086/rPorA Mixing Study – WCE Titers

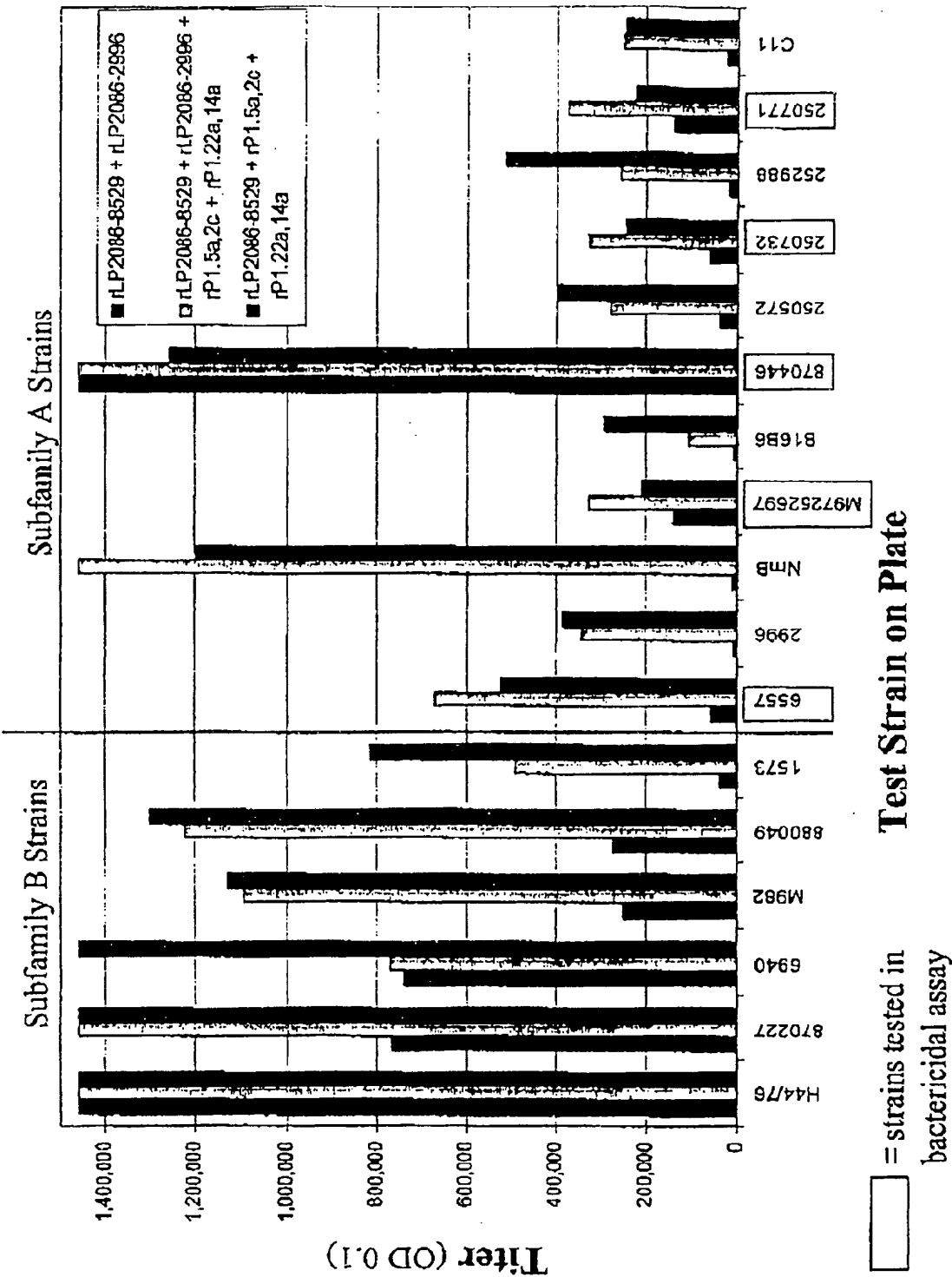
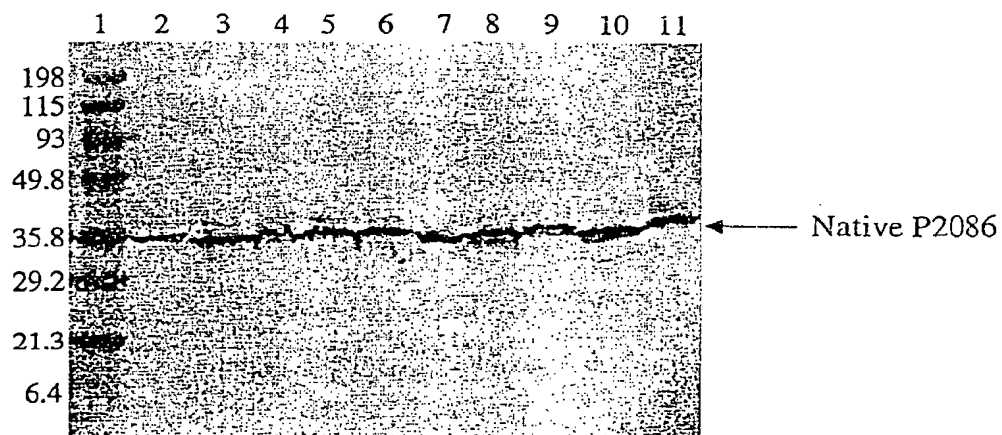


FIG. 16

Western Blot Reactivity of rLP2086 Mouse Antisera to P2086 Subfamily B *N. meningitidis* Whole Cell Lysates

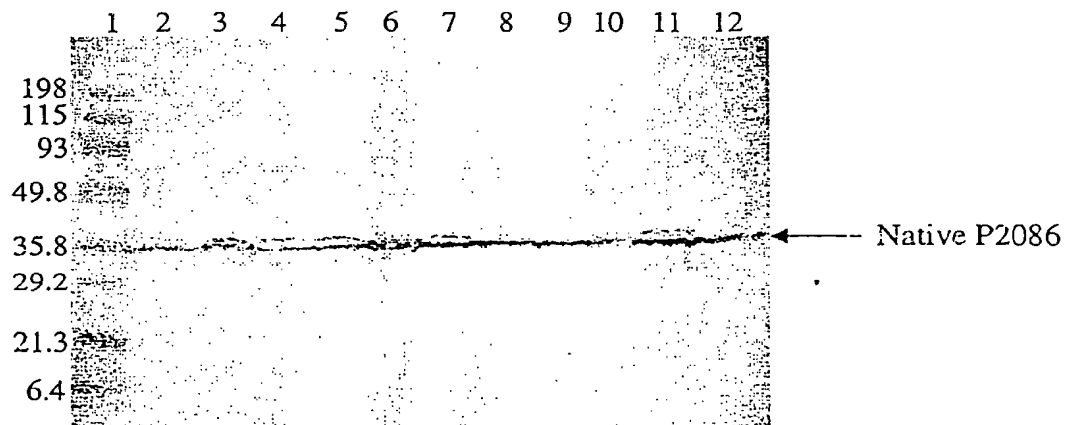


1 – Molecular Weight Marker (kDa)	7 – CDC1359
2 – M97 251985	8 – CDC1658
3 – CDC937	9 – M97 252026
4 – 6940	10 – M97 252029
5 – M97 251926	11 – M982
6 – CDC1573	

Subfamily B P2086 cell lysates are all Group B *N. meningitidis*

FIG. 17

Western Blot Reactivity of rLP2086 Mouse Antisera to
P2086 Subfamily A *N. meningitidis* and *N. lactamica*
Whole Cell Lysates



1 – Molecular Weight Markers (kDa)
2 – Group A *N. meningitidis* A4 (P2086 Subfamily B)
3 – Group C *N. meningitidis* - C11
4 – Group Y *N. meningitidis* - ATCC35561
5 – Group W135 *N. meningitidis* - ΔTCC35559
6 – *N. lactamica* - UR5

Group B *N. meningitidis*:
7 – CDC1034
8 – M98 250732
9 – NmB
10 – 6557
11 – CDC1521
12 – M97 252153

FIG. 18

SEQUENCE LISTING

<110> Zlotnick, Gary
 Fletcher, Leah
 John, Farley
 Bernfield, Liesel
 Zagursky, Robert
 Metcalf, Benjamin

<120> Novel Immunogenic Compositions for the Prevention and Treatment of
 Meningococcal Disease

<130> 38523.000016

<150> US 60/328,101

<151> 2001-10-11

<150> US 60/406,934

<151> 2002-08-30

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<170> PatentIn version 3.1

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 20 25 30

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 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly
 165 170 175

Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
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 <211> 255
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 20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
 35 40 45

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80

Arg Gln Ile Glu Val Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu
 85 90 95

Phe Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val Ala Leu Gln Ile
 100 105 110

Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
 115 120 125

Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln
 130 135 140

Leu Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp
 145 150 155 160

Asp Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln
 165 170 175

Gly Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu
 180 185 190

Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile
 195 200 205

Leu Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu
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 accacaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc 120
 aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc 180
 gacagcctca atacgggcaa attgaagaac gacaaggcca gccgcttcga ctttatccgt 240
 caaatcgaag tggacggaca aaccatcacg ctggcaagcg gcgaatttca aatatacaaa 300
 cagaaccact ccgccgtcgt tgccttacag attgaaaaaa tcaacaaccc cgacaaaatc 360
 gacagcctga taaaccaacg ctcttcctt gtcagcgggt tgggcggaga acataccgcc 420
 ttcaaccaac tgctgacgg caaagccgag tatcacggca aagcattcag ctccgacgac 480
 ccgaacggca ggctgcacta ctccattgat ttacacaaaa aacaggggta cggcagaatc 540
 gaacacctga aaacgcccga gcagaatgtc gagcttgctt ccgccgaact caaagcagat 600
 gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact 660
 taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag 720
 ataagggaaa aggttcacga aatcggcatc gccggcaaac agtag 765

<210> 6
 <211> 254
 <212> PRT
 <213> Neisseria meningitidis

<400> 6
 Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15
 Ala Asp Ala Leu Thr Thr Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30
 Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45
 Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn

6

50 55 60
 Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80
 Gln Ile Glu Val Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe
 85 90 95
 Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110
 Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125
 Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140
 Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160
 Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly
 165 170 175
 Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190
 Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205
 Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220
 Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240
 Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 7
 <211> 765
 <212> DNA
 <213> Neisseria meningitidis
 <400> 7


```

tgcagcagcg gagggcggcgg tgtcgccgcc gacatcggcg cggggccttgc cgatgcacta      60
accacaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc      120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc      180
gacagcctca atacgggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt      240
caaatcgaag tggacggaca aaccatcacg ctggcaagcg gcgaatttca aatatacaaa      300
cagaaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc      360
gacagcctga taaaccaacg ctccctcctt gtcagcgggt tgggcggaga acataccgcc      420
ttcaaccaac tgcttgacgg caaagccgag tatcacggca aagcattcag ctccgacgac      480
ccgaacggca ggctgcacta ctccattgat ttaccaaaaa aacaggggta cggcagaatc      540
gaacacctga aaacgcccga gcagaatgtc gagcttgctt ccgccgaact caaagcagat      600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact      660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggcccggc aaccgtgaag      720
ataagggaaa aggttcacga aatcggcatc gccagcaaac agtag                        765

```

```

<210> 8
<211> 254
<212> PRT
<213> Neisseria meningitidis

```

```

<400> 8

```

```

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10          15

```

```

Ala Asp Ala Leu Thr Thr Pro Leu Asp His Lys Asp Lys Ser Leu Gln
          20          25          30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
35          40          45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
50          55          60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65          70          75          80

```

```

Gln Ile Glu Val Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe
          85          90          95

```


Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly
 165 170 175

Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Pro Ala Thr Val Lys
 225 230 235 240

Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Ser Lys Gln
 245 250

<210> 9

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 9

tgcg gatcca gcggaggcgg cgggtgtcgcc gccgacatcg gcgcggggct tgccgatgca 60

ctaaccacac cgctcgacca taaagacaaa agtttgcagt ctttgacgct ggatcagtcc 120

gtcaggaaaa acgagaaaact gaagctggcg gcacaagggtg cggaaaaaac ttatggaaac 180

ggcgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgctt cgactttatc 240

cgtcaaatcg aagtggacgg acaaaccatc acgctggcaa gcggcgaatt tcaaatatac 300


```

aacagaacc actccgccgt cgttgcccta cagattgaaa aaatcaacaa ccccgacaaa   360
atcgacagcc tgataaacca acgctccttc cttgtcagcg gtttgggagg agaacatacc   420
gccttcaacc aactgcctga cggcaaagcc gagtatcacg gcaaagcatt cagctccgac   480
gacccgaacg gcaggetgca ctactccatt gattttacca aaaaacaggg ttacggcaga   540
atcgaacacc tgaaaacgcc cgagcagaat gtcgagcttg cctccgccga actcaaagca   600
gatgaaaaat cacacgccgt cattttgggc gacacgcgct acggcgggcg agaaaaaggc   660
acttaccacc tcgccctttt cggcgaccgc gcccaagaaa tcgccggccc ggcaaccgtg   720
aagataaggg aaaaggttca cgaaatcggc atcgccagca aacagtag               768

```

```

<210> 10
<211> 255
<212> PRT
<213> Neisseria meningitidis

```

```

<400> 10

```

```

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
1           5           10           15

```

```

Leu Ala Asp Ala Leu Thr Thr Pro Leu Asp His Lys Asp Lys Ser Leu
          20           25           30

```

```

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
          35           40           45

```

```

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
          50           55           60

```

```

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
65           70           75           80

```

```

Arg Gln Ile Glu Val Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu
          85           90           95

```

```

Phe Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val Ala Leu Gln Ile
          100          105          110

```

```

Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
          115          120          125

```

```

Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln

```


130 135 140
 Leu Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp
 145 150 155 160
 Asp Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln
 165 170 175
 Gly Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu
 180 185 190
 Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile
 195 200 205
 Leu Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu
 210 215 220
 Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Pro Ala Thr Val
 225 230 235 240
 Lys Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Ser Lys Gln
 245 250 255

<210> 11
 <211> 765
 <212> DNA
 <213> Neisseria meningitidis

<400> 11
 atgagcagcg gagggcggcg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta 60
 accacaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc 120
 aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc 180
 gacagcctca atacgggcaa attgaagaac gacaaggcca gccgcttoga ctttatccgt 240
 caaatcgaag tggacggaca aaccatcacg ctggcaagcg gccaatttca aatatacaaa 300
 cagaaccact ccgccgtcgt tgcctacag attgaaaaaa tcaacaaccc cgacaaaatc 360
 gacagcctga taaaccaacg ctcttctctt gtcagcgggt tgggcggaga acataccgcc 420
 ttcaaccaac tgctgacgg caaagccgag tatcacggca aagcattcag ctccgacgac 480
 ccgaacggca ggctgcacta ctccattgat ttacaaaaa aacagggtta cggcagaatc 540
 gaacacctga aaacgcccga gcagaatgtc gagcttgctt ccgccgaact caaagcagat 600

gaaaaatcac acgccgtcat ttggggcgac acgcgctacg gcggcgaaga aaaaggcact 660
 taccacctcg ccccttttcgg cgaccgcgcc caagaaatcg ccggcccggc aaccgtgaag 720
 ataagggaaa aggttcacga aatcggcatc gccagcaaac agtag 765

<210> 12
 <211> 254
 <212> PRT
 <213> Neisseria meningitidis

<400> 12

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Thr Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly
 165 170 175

Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Pro Ala Thr Val Lys
 225 230 235 240

Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Ser Lys Gln
 245 250

<210> 13

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 13

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tgcagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcgcgtc      120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc      180
gacagcctca atacgggcaa attgaagaac gacaaggcca gccgcttcga ctttatccgt      240
caaatcggag tggacggaca aaccatcacg ctggcaagcg gcgaatttca aatatacaaa      300
cagaaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc      360
gacagcctga taaaccaacg ctccctcctt gtcagcgggt tgggcggaga acataccgcc      420
ttcaaccaac tgctgacgg caaagccgag tatcacggca aagcattcag ctccgacgac      480
ccgaacggca ggctgcacta ctccattgat ttaccaaaaa aacagggtta cggcagaatc      540
gaacacctga aaacgcccga gcagaatgtc gagcttgccct ccgccgaact caaagcagat      600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact      660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag      720
ataagggaaa aggttcacga aatcggcatc gccggcaaac agtag                          765

```

<210> 14

<211> 254

<212> PRT

<213> Neisseria meningitidis

<400> 14

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Gly Val Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly
 165 170 175

Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala

14

210	215	220
Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys		
225	230	235 240
Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln		
	245	250

<210> 15
 <211> 768
 <212> DNA
 <213> Neisseria meningitidis

<400> 15
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 ctaaccgcac cgctcgacca taaagacaaa agtttgcagt ctttgacgct ggatcagtcc 120
 gtcaggaaaa acgagaaaact gaagctggcg gcacaagggtg cggaaaaaac ttatggaaac 180
 ggcgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgctt cgactttatc 240
 cgtcaaatacg gagtggacgg acaaaccatc acgctggcaa gcggcgaatt tcaaataatc 300
 aaacagaacc actccgccgt cgttgcccta cagattgaaa aaatcaacaa ccccgacaaa 360
 atcgacagcc tgataaacca acgctccttc cttgtcagcg gtttggggcg agaacatacc 420
 gccttcaacc aactgcctga cggcaaagcc gagtatcacg gcaaagcatt cagctccgac 480
 gaccgaacg gcaggctgca ctactccatt gattttacca aaaaacaggg ttacggcaga 540
 atcgaacacc tgaaaacgcc cgagcagaat gtcgagcttg cctccgccga actcaaagca 600
 gatgaaaaat cacacgccgt cattttgggc gacacgcgct acggcgggcg agaaaaaggg 660
 acttaccacc tcgccctttt cggcgaccgc gcccaagaaa tcgccggctc ggcaaccgtg 720
 aagataaggg aaaagggttca cgaaatcggc atcgccggca aacagtag 768

<210> 16
 <211> 255
 <212> PRT
 <213> Neisseria meningitidis

<400> 16
 Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
 20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
 35 40 45

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80

Arg Gln Ile Gly Val Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu
 85 90 95

Phe Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val Ala Leu Gln Ile
 100 105 110

Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
 115 120 125

Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln
 130 135 140

Leu Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp
 145 150 155 160

Asp Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln
 165 170 175

Gly Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu
 180 185 190

Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile
 195 200 205

Leu Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu
 210 215 220

Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val
 225 230 235 240

Lys Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250 255

<210> 17
 <211> 765
 <212> DNA
 <213> *Neisseria meningitidis*

<400> 17
 atgagcagcg gagggcggcg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta 60
 accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc 120
 aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc 180
 gacagcctca atacgggcaa attgaagaac gacaaggcca gccgcttcga ctttatccgt 240
 caaatcggag tggacggaca aaccatcacg ctggcaagcg gcgaatttca aatatacaaa 300
 cagaaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc 360
 gacagcctga taaaccaacg ctcttctctt gtcagcgggt tgggcggaga acataccgcc 420
 ttcaaccaac tgccctgacg caaagccgag tatcacggca aagcattcag ctccgacgac 480
 ccgaacggca ggctgcacta ctccattgat ttaccacaaa aacagggtta cggcagaatc 540
 gaacacctga aaacgcccga gcagaatgtc gagcttgcc tccgccgaact caaagcagat 600
 gaaaaatcac acgccgtcat tttggggcgac acgcgctacg gcggcgaaga aaaaggcact 660
 taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag 720
 ataagggaaa aggttcacga aatcggcatc gccggcaaac agtag 765

<210> 18
 <211> 254
 <212> PRT
 <213> *Neisseria meningitidis*

<400> 18
 Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15
 Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30
 Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45
 Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

17

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65 70 75 80

Gln Ile Gly Val Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe
85 90 95

Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val Ala Leu Gln Ile Glu
100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
130 135 140

Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
145 150 155 160

Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly
165 170 175

Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
180 185 190

Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
195 200 205

Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
225 230 235 240

Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
245 250

<210> 19

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 19

tgcagcagca gaggcggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta 60

accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcgcgc 120


```

aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc   180
gacagcctca atacgggcaa attgaagaac gacaagggtca gccgcttcga ctttatccgt   240
caaatcgaag tggacggaca aaccatcacg ctggcaagcg gcgaatttca aatatacaaaa   300
cagaaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc   360
gacagcctga taaaccaacg ctccctcctt gtcagcgggt tgggcggaga acataccgcc   420
ttcaaccaac tgctgacgg caaagccgag tatcacggca aagcattcag ctccgacgac   480
ccgaacggca ggctgacta ctccattgat ttaccaaaa aacagggtta cggcagaatc   540
gaacacctga aaacgcccga gcagaatgtc gagcttgctt ccgccgaact caaagcagat   600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact   660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag   720
ataagggaag aggttcacga aatcggcatc gccggcaaac agtag                       765

```

```

<210> 20
<211> 254
<212> PRT
<213> Neisseria meningitidis

<400> 20

```

```

Cys Ser Ser Arg Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10          15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
          20          25          30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35          40          45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50          55          60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65          70          75          80

```

```

Gln Ile Glu Val Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe
          85          90          95

```

```

Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val Ala Leu Gln Ile Glu
          100         105         110

```


Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly
 165 170 175

Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 21

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 21

tgccgatcca gcagagggcg cgggtgtcgcc gccgacatcg gcgcgggggct tgccgatgca 60

ctaaccgcac cgctcgacca taaagacaaa agtttgcagt ctttgacgct ggatcagtc 120

gtcaggaaaa acgagaaaact gaagctggcg gcacaagggt cggaaaaaac ttatggaaac 180

ggcgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgctt cgactttatc 240

cgtcaaatcg aagtggacgg acaaaccatc acgctggcaa gcggcggaatt tcaaatatac 300

aaacagaacc actccgccgt cgttgcccta cagattgaaa aaatcaacaa ccccgacaaa 360

atcgacagcc tgataaacca acgctccttc cttgtcagcg gtttggggcg agaacatacc 420


```

gccttcaacc aactgcctga cggcaaagcc gagtatcacg gcaaagcatt cagctccgac    480
gacctgaacg gcaggctgca ctactccatt gattttacca aaaaacaggg ttacggcaga    540
atcgaacacc tgaaaacgcc cgagcagaat gtcgagcttg cctccgccga actcaaagca    600
gatgaaaaat cacacgccgt cattttgggc gacacgcgct acggcggcga agaaaaaggc    660
acttaccacc tcgccctttt cggcgaccgc gccaagaaa tcgccggctc ggcaaccgtg    720
aagataaggg aaaaggttca cgaaatcggc atcgccggca aacagtag                768

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<210> 22

<211> 255

<212> PRT

<213> Neisseria meningitidis

<400> 22

```

Cys Gly Ser Ser Arg Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
1           5           10           15

```

```

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
          20           25           30

```

```

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
          35           40           45

```

```

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
          50           55           60

```

```

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
65           70           75           80

```

```

Arg Gln Ile Glu Val Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu
          85           90           95

```

```

Phe Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val Ala Leu Gln Ile
          100          105          110

```

```

Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
          115          120          125

```

```

Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln
          130          135          140

```


21

Leu Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp
 145 150 155 160

Asp Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln
 165 170 175

Gly Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu
 180 185 190

Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile
 195 200 205

Leu Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu
 210 215 220

Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val
 225 230 235 240

Lys Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250 255

<210> 23

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 23

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atgagcagca gaggcggcgg tgcgcgccgc gacatcgggc cggggccttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc      120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc      180
gacagcctca atacgggcaa attgaagaac gacaaggcca gccgcttcga ctttatccgt      240
caaatcgaag tggacggaca aaccatcacg ctggcaagcg gcgaatttca aatatacaaa      300
cagaaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc      360
gacagcctga taaaccaacg ctcttcctt gtcagcgggt tgggcggaga acataccgcc      420
ttcaaccaac tgctgacgg caaagccgag tatcacggca aagcattcag ctccgacgac      480
ccgaacggca ggctgcacta ctccattgat ttaccaaaa aacaggggta cggcagaatc      540
gaacacctga aaacgcccga gcagaatgtc gagcttgctt ccgccgaact caaagcagat      600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gggcggaaga aaaaggcact      660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag      720

```


ataagggaaa aggttcacga aatcggcacg gccggcaaac agtag

765

<210> 24

<211> 254

<212> PRT

<213> Neisseria meningitidis

<400> 24

Met Ser Ser Arg Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65 70 75 80

Gln Ile Glu Val Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe
85 90 95

Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val Ala Leu Gln Ile Glu
100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
130 135 140

Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
145 150 155 160

Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly
165 170 175

Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
180 185 190

Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 25

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 25

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tgcagcagcg gaggcggcgg tgctgcgcgc gacatcggcg cggggccttgc cgatgcacta      60
accgcaccgt tgcaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcgcgc      120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc      180
gacagcctca atacgggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt      240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa      300
caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc      360
gacagcctga taaaccaacg ctcccttctt gtcagcgggt tgggtggaga acataccgcc      420
ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgac      480
ccgaacggca ggctgcacta ctccattgat ttaccaaaaa aacagggtta cggcagaatc      540
gaacacctga aaacgcccga gcagaatgtc gagcttgctt ccgccgaact caaagcagat      600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact      660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag      720
ataagggaaa aggttcacga aatcggcatc gccggcaaac agtag                          765

```

<210> 26

<211> 254

<212> PRT

<213> Neisseria meningitidis

<400> 26

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15
 Ala Asp Ala Leu Thr Ala Pro Phe Asp His Lys Asp Lys Ser Leu Gln
 20 25 30
 Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45
 Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60
 Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80
 Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95
 Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110
 Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125
 Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140
 Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160
 Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly
 165 170 175
 Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190
 Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205
 Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

25

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 27
 <211> 768
 <212> DNA
 <213> Neisseria meningitidis

<400> 27
 tgcggatcca gcggaggcgg cgggtgtcgcc gccgacatcg gcgcggggct tgccgatgca 60
 ctaaccgcac cgttcgacca taaagacaaa agtttgcagt ctttgacgct ggatcagtc 120
 gtcaggaaaa acgagaaact gaagctggcg gcacaaggtg cggaaaaaac ttatggaaac 180
 ggcgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgctt cgactttatc 240
 cgtcaaactg aagtggacgg gcagctcatt accttgagaga gcggagagtt ccaaataac 300
 aaacaggacc actccgccgt cgttgcccta cagattgaaa aaatcaacaa ccccgacaaa 360
 atcgacagcc tgataaacca acgctccttc cttgtcagcg gtttgggtgg agaacatacc 420
 gccttcaacc aactgccag cggcaaagcc gagtatcacg gcaaagcatt cagctccgac 480
 gacccgaacg gcaggctgca ctactccatt gattttacca aaaaacaggg ttacggcaga 540
 atcgaacacc tgaaaacgcc cgagcagaat gtcgagcttg cctccgccga actcaaagca 600
 gatgaaaaat cacacgccgt cttttgggc gacacgcgt acggcggcga agaaaaaggc 660
 acttaccacc tcgccctttt cggcgaccgc gcccaagaaa tcgccggctc ggcaaccgtg 720
 aagataaggg aaaaggttca cgaaatcggc atcgccggca aacagtag 768

<210> 28
 <211> 255
 <212> PRT
 <213> Neisseria meningitidis

<400> 28

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Phe Asp His Lys Asp Lys Ser Leu
 20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys

35	40	45
Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu		
50	55	60
Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile		
65	70	75 80
Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu		
	85	90 95
Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile		
	100	105 110
Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg		
	115	120 125
Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln		
	130	135 140
Leu Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp		
145	150	155 160
Asp Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln		
	165	170 175
Gly Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu		
	180	185 190
Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile		
	195	200 205
Leu Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu		
	210	215 220
Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val		
225	230	235 240
Lys Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln		
	245	250 255

<210> 29

<211> 765

<212> DNA

<213> *Neisseria meningitidis*

<400> 29

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atgagcagcg gaggcggcgg tgcgcgccgc gacatcggcg cggggccttgc cgatgcacta      60
accgcaccgt tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc      120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc      180
gacagcctca atacgggcaa attgaagaac gacaagggtca gccgcttcga ctttatccgt      240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa      300
caggaccact ccgccgtcgt tgccttacag attgaaaaaa tcaacaaccc cgacaaaatc      360
gacagcctga taaaccaacg ctcccttctt gtcagcgggt tgggtggaga acataccgcc      420
ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgac      480
ccgaacggca ggctgcacta ctccattgat ttaccaaaaa aacaggggta cggcagaatc      540
gaacacctga aaacgcccga gcagaatgtc gagcttgctt ccgccgaact caaagcagat      600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact      660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag      720
ataagggaaa aggttcacga aatcggcatc gccggcaaac agtag                          765

```

<210> 30

<211> 254

<212> PRT

<213> *Neisseria meningitidis*

<400> 30

```

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10           15

```

```

Ala Asp Ala Leu Thr Ala Pro Phe Asp His Lys Asp Lys Ser Leu Gln
          20           25           30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35           40           45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50           55           60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65           70           75           80

```


Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly
 165 170 175

Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 31

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 31

tgcagcagcg gaggcggcgg tgtcgccgcc gacatcgggc cggggcttgc cgatgcacta 60

accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcgcgc 120

aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc 180


```

gacagcctca atacgggcaa attgaagaac gacaagggtca gccgcttcga ctttatccgt      240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaaa      300
caggaccact ccgccgtcgt tgccttacag attgaaaaaa tcaacaaccc cgacaaaatc      360
gacagcctga taaaccaacg ctcccttcctt gtcagcggtt tgggtggaga acataccgcc      420
ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgac      480
ccgaacggca ggctgcaact ctccattgat tttaacaaaa aacagggtta cggcagaatc      540
gaacacctga aaacgcccga gcagaatgtc gagcttgctt ccgccgaact caaagcagat      600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact      660
taccacctcg ccccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag      720
ataagggaaa aggttcacga aatcggcacg gccggcaaac agtag                          765

```

```

<210> 32
<211> 254
<212> PRT
<213> Neisseria meningitidis

```

```

<400> 32

```

```

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10           15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
          20           25           30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35           40           45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50           55           60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65           70           75           80

```

```

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
          85           90           95

```

```

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
          100          105          110

```

```

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser

```


115 120 125
 Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140
 Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160
 Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly
 165 170 175
 Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190
 Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205
 Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220
 Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240
 Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 33

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 33

tgcggatcca gcggaggcgg cgggtgtcgcc gccgacatcg gcgcggggct tgccgatgca 60
 ctaaccgcac cgctcgacca taaagacaaa agtttgcagt ctttgacgct ggatcagtcc 120
 gtcaggaaaa acgagaaaact gaagctggcg gcacaagggtg cggaaaaaac ttatggaaac 180
 ggcgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgctt cgactttatc 240
 cgtcaaatacg aagtggacgg gcagctcatt accttggaga gcggagagtt ccaaataac 300
 aaacaggacc actccgccgt cgttgcccta cagattgaaa aaatcaacaa ccccgacaaa 360
 atcgacagcc tgataaacca acgctccttc cttgtcagcg gtttgggtgg agaacatacc 420
 gccttcaacc aactgcccag cggcaaagcc gagtatcacg gcaaagcatt cagctccgac 480


```

gacccgaacg gcaggctgca ctactccatt gattttacca aaaaacaggg ttacggcaga      540
atcgaacacc tgaaaacgcc cgagcagaat gtcgagcttg cctccgccga actcaaagca      600
gatgaaaaat cacacgccgt cattttgggc gacacgcgct acggcgccga agaaaaaggc      660
acttaccacc tcgccctttt cggcgaccgc gcccaagaaa tcgccggctc ggcaaccgtg      720
aagataaggg aaaaggttca cgaaatcggc atcgccggca aacagtag                    768

```

```

<210> 34
<211> 255
<212> PRT
<213> Neisseria meningitidis

```

```

<400> 34

```

```

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
1           5           10           15

```

```

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
          20           25           30

```

```

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
      35           40           45

```

```

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
      50           55           60

```

```

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
65           70           75           80

```

```

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
      85           90           95

```

```

Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile
      100          105          110

```

```

Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
      115          120          125

```

```

Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln
      130          135          140

```

```

Leu Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp
145          150          155          160

```


Asp Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln
 165 170 175

Gly Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu
 180 185 190

Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile
 195 200 205

Leu Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu
 210 215 220

Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val
 225 230 235 240

Lys Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250 255

<210> 35

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 35

atgagcagcg gagggcgcgg tgtcgccgcc gacatcgggc cggggcttgc cgatgcacta	60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcgctc	120
aggaaaaacg agaaactgaa gctggcgggc caaggtgcgg aaaaaactta tggaaacggc	180
gacagcctca atacgggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt	240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa	300
caggaccact ccgccgtcgt tgccttacag attgaaaaaa tcaacaaccc cgacaaaatc	360
gacagcctga taaaccaacg ctccctcctt gtcagcgggt tgggtggaga acataccgcc	420
ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgac	480
ccgaacggca ggctgcacta ctccattgat ttaccaaaa aacagggtta cggcagaatc	540
gaacacctga aaacgcccga gcagaatgtc gagcttgctt ccgccgaact caaagcagat	600
gaaaaatcac acgccgtcat tttggggcgac acgcgctacg gcggcgaaga aaaaggcact	660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag	720
ataagggaaa aggttcacga aatcggcatc gccggcaaac agtag	765

<210> 36
 <211> 254
 <212> PRT
 <213> *Neisseria meningitidis*

 <400> 36

 Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

 Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

 Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

 Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

 Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

 Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

 Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

 Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

 Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

 Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

 Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly
 165 170 175

 Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

 Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu

195	200	205
Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala		
210	215	220
Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys		
225	230	235 240
Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln		
245	250	

<210> 37
 <211> 765
 <212> DNA
 <213> Neisseria meningitidis

<400> 37
 tgcagcagcg gagggcgcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta 60
 accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcgcgc 120
 aggaaaaacg agaaactgaa gctggcgggc caaggtgcgg aaaaaactta tggaaacggc 180
 gacagcctca atacggggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt 240
 caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa 300
 caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc 360
 gacagcctga taaaccaacg ctcccttctt gtcagcggtt tgggtggaga acataccgcc 420
 ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgac 480
 ccgaacggca ggctgcacta ctccattgat tttacaaaaa aacaggggta cggcagaatc 540
 gaacacctga aaacgcccga gcagaatgtc gagcttgctt ccgccgaact caaagcagat 600
 gaaaaatcac acgccgtcat tttggggcgac acgcgctacg gcggcgaaga aaaaggcact 660
 taccacctcg ccccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag 720
 ataagggaaa aggttcacga aatcggcatc gccggcaaac agtag 765

<210> 38
 <211> 254
 <212> PRT
 <213> Neisseria meningitidis

<400> 38
 Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly
 165 170 175

Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
245 250

```
<210> 39
<211> 768
<212> DNA
<213> Neisseria meningitidis
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<400>	39						
tgcggatcca	gcggagggcgg	cggtgtcgcc	gccgacatcg	gcgcgggggct	tgccgatgca		60
ctaaccgcac	cgctcgacca	taaagacaaa	agtttgcagt	ctttgacgct	ggatcagtc		120
gtcaggaaaa	acgagaaact	gaagctggcg	gcacaagggtg	cggaaaaaac	ttatggaaac		180
ggcgacagcc	tcaatacggg	caaattgaag	aacgacaagg	tcagccgctt	cgactttatc		240
cgtcaaatac	aagtggacgg	gcagctcatt	accttgga	gcggagagtt	ccaaatatac		300
aaacaggacc	actccgccgt	cgttgcccta	cagattgaaa	aatcaacaa	ccccgacaaa		360
atcgacagcc	tgataaacca	acgctccttc	cttgtcagcg	gtttgggtgg	agaacatacc		420
gccttcaacc	aactgcccag	cggcaaagcc	gagtatcacg	gcaaagcatt	cagctccgac		480
gacccgaacg	gcaggctgca	ctactccatt	gattttacca	aaaaacaggg	ttacggcaga		540
atcgaacacc	tgaaaacgcc	cgagcagaat	gtcgagcttg	cctccgccga	actcaaagca		600
gatgaaaaat	cacacgccgt	cattttgggc	gacacgcgct	acggcggcga	agaaaaaggc		660
acttaccacc	tcgccctttt	cggcgaccgc	gcccagaaga	tcgccggctc	ggcaaccgtg		720
aagataaggg	aaaagggttc	cgaaatcggc	atcgccggca	aacagtag			768

```
<210> 40
<211> 255
<212> PRT
<213> Neisseria meningitidis
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<400> 40

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
35 40 45

37

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
 85 90 95

Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile
 100 105 110

Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
 115 120 125

Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln
 130 135 140

Leu Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp
 145 150 155 160

Asp Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln
 165 170 175

Gly Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu
 180 185 190

Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile
 195 200 205

Leu Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu
 210 215 220

Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val
 225 230 235 240

Lys Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250 255

<210> 41

<211> 765

<212> DNA

<213> Neisseria meningitidis


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<400> 41
atgagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc      120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc      180
gacagcctca atacgggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt      240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa      300
caggaccact ccgcgctcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc      360
gacagcctga taaaccaacg ctcttctcct gtcagcgggt tgggtggaga acataccgcc      420
ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgac      480
ccgaacggca ggctgcacta ctccattgat ttaccaaaaa aacagggtta cggcagaatc      540
gaacacctga aaacgcccga gcagaatgtc gagcttgctt ccgccgaact caaagcagat      600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact      660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag      720
ataagggaaa aggttcacga aatcggcacg gccggcaaac agtag                          765

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<210> 42
<211> 254
<212> PRT
<213> Neisseria meningitidis

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```

<400> 42

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1          5          10          15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
          20          25          30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35          40          45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50          55          60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65          70          75          80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
          85          90          95

```


Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly
 165 170 175

Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 43

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 43

tgcagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta 60

accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc 120

aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc 180

gacagcctca atacgggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt 240

caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa 300


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caggaccact ccgccgtcgt tgcctacag attgaaaaaa tcaacaaccc cgacaaaatc 360
gacagcctga taaaccaacg ctccttcctt gtcagcgggt tgggtggaga acataccgcc 420
ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgac 480
ccgaacggca ggctgcaact ctccattgat ttaccacaaa aacaggggta cggcagaatc 540
gaacacctga aaacgcccga gcagaatgtc gagcttgctt ccgccgaact caaagcagat 600
gaaaaatcac acgccgtcat tttggggcgac acgcgctacg gcggcgaaga aaaaggcact 660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag 720
ataagggaaa aggttcacga aatcggcatc gccggcaaac agtag 765

```

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<210> 44
<211> 254
<212> PRT
<213> Neisseria meningitidis

<400> 44

```

```

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10           15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
          20           25           30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35           40           45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50           55           60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65           70           75           80

```

```

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
          85           90           95

```

```

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
          100          105          110

```

```

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
          115          120          125

```


Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly
 165 170 175

Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 45
 <211> 768
 <212> DNA
 <213> Neisseria meningitidis

<400> 45
 tgcggatcca gcggaggcgg cgggtgtcgcc gccgacatcg gcgcgggggct tgccgatgca 60
 ctaaccgcac cgctcgacca taaagacaaa agtttgcagt ctttgacgct ggatcagtc 120
 gtcaggaaaa acgagaaact gaagctggcg gcacaagggt cggaaaaaaac ttatggaaac 180
 ggcgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgctt cgactttatc 240
 cgtcaaatacg aagtggacgg gcagctcatt accttgagga gcggagagtt ccaaataatac 300
 aaacaggacc actccgccgt cgttgcccta cagattgaaa aaatcaacaa ccccgacaaa 360
 atcgacagcc tgataaacca acgctccttc cttgtcagcg gtttgggtgg agaacatacc 420
 gccttcaacc aactgcccag cggcaaagcc gagtatcacg gcaaagcatt cagctccgac 480
 gacccgaacg gcaggctgca ctactccatt gattttacca aaaaacaggg ttacggcaga 540
 atcgaacacc tgaaaacgcc cgagcagaat gtcgagcttg cctccgccga actcaaagca 600

gatgaaaaat cacacgccgt cattttgggc gacacgcgct acggcggcga agaaaaaggc 660
 acttaccacc tcgccctttt cggcgaccgc gcccaagaaa tcgccggctc ggcaaccgtg 720
 aagataaggg aaaaggttca cgaaatcggc atcgccggca aacagtag 768

<210> 46
 <211> 255
 <212> PRT
 <213> Neisseria meningitidis

<400> 46

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
 20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
 35 40 45

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
 85 90 95

Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile
 100 105 110

Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
 115 120 125

Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln
 130 135 140

Leu Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp
 145 150 155 160

Asp Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln
 165 170 175

Gly Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu
 180 185 190

Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile
 195 200 205

Leu Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu
 210 215 220

Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val
 225 230 235 240

Lys Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250 255

<210> 47

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 47

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atgagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcgcgc      120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc      180
gacagcctca atacgggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt      240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa      300
caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc      360
gacagcctga taaaccaacg ctccctcctt gtcagcgggt tgggtggaga acataccgcc      420
ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgac      480
ccgaacggca ggctgcacta ctccattgat tttacaaaaa aacaggggta cggcagaatc      540
gaacacctga aaacgcccga gcagaatgtc gagcttgctt ccgccgaact caaagcagat      600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact      660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag      720
ataagggaaa aggttcacga aatcggcatc gccggcaaac agtag                          765

```

<210> 48

<211> 254

44

<212> PRT

<213> Neisseria meningitidis

<400> 48

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly
 165 170 175

Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

45

Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 49

<211> 786

<212> DNA

<213> Neisseria meningitidis

<400> 49

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tgcagcagcg gaagcggaag cggaggcggc ggtgtcgccg ccgacatcgg cacagggctt      60
gccgatgcac taactgcgcc gctcgaccat aaagacaaag gtttgaaatc cctgacattg      120
gaagactcca tttcccaaaa cggaacactg accctgtcgg cacaaggtgc ggaaaaaact      180
ttcaaagtcg gcgacaaaga caacagtctc aatacaggca aattgaagaa cgacaaaatc      240
agccgcttcg actttgtgca aaaaatcgaa gtggacggac aaaccatcac gctggcaagc      300
ggcgaatttc aaatatacaa acaggaccac tccgccgtcg ttgccctaca gattgaaaaa      360
atcaacaacc ccgacaaaat cgacagcctg ataaaccaac gctccttcct tgtcagcggc      420
ttgggcgagg aacataccgc cttcaaccaa ctgccacgag gcaaagccga gtatcacggc      480
aaagcattca gctccgacga tgccggcgga aaactgacct ataccataga ttttgccgcc      540
aaacagggac acggcaaaaat cgaacacctg aaaacacccg agcagaatgt cgagcttgcc      600
tccgccgaac tcaaagcaga tgaaaaatca cagccgtca ttttgggcga cacgcgtac      660
ggcagcgaag aaaaaggcac ttaccacctc gctcttttcg gcgaccgagc ccaagaaatc      720
gccggctcgg caaccgtgaa gataagggaa aaggttcacg aaatcggcac cgccggcaaa      780
cagtag                                           786
  
```

<210> 50

<211> 261

<212> PRT

<213> Neisseria meningitidis

<400> 50

Cys Ser Ser Gly Ser Gly Ser Gly Gly Gly Gly Val Ala Ala Asp Ile
 1 5 10 15

Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp
 20 25 30

Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn Gly
 35 40 45

Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Val Gly
 50 55 60

Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile
 65 70 75 80

Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr Ile
 85 90 95

Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser Ala
 100 105 110

Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp
 115 120 125

Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly Glu
 130 135 140

His Thr Ala Phe Asn Gln Leu Pro Ser Gly Lys Ala Glu Tyr His Gly
 145 150 155 160

Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile
 165 170 175

Asp Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr
 180 185 190

Pro Glu Gln Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu
 195 200 205

Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu
 210 215 220

Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile
 225 230 235 240

Ala Gly Ser Ala Thr Val Lys Ile Arg Glu Lys Val His Glu Ile Gly
245 250 255

Ile Ala Gly Lys Gln
260

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<210> 51
<211> 789
<212> DNA
<213> Neisseria meningitidis
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[illegible]

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<210> 52
<211> 262
<212> PRT
<213> Neisseria meningitidis
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<400> 52

Cys Gly Ser Ser Gly Ser Gly Ser Gly Gly Gly Gly Val Ala Ala Asp
1 5 10 15

Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys
20 25 30

Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn
 35 40 45

Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Val
 50 55 60

Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys
 65 70 75 80

Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr
 85 90 95

Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser
 100 105 110

Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile
 115 120 125

Asp Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly
 130 135 140

Glu His Thr Ala Phe Asn Gln Leu Pro Ser Gly Lys Ala Glu Tyr His
 145 150 155 160

Gly Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr
 165 170 175

Ile Asp Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys
 180 185 190

Thr Pro Glu Gln Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala Asp
 195 200 205

Glu Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu
 210 215 220

Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu
 225 230 235 240

Ile Ala Gly Ser Ala Thr Val Lys Ile Arg Glu Lys Val His Glu Ile
 245 250 255

Gly Ile Ala Gly Lys Gln
260

<210> 53
<211> 786
<212> DNA
<213> *Neisseria meningitidis*

<400> 53
atgagcagcg gaagcggaag cggaggcggc ggtgtcgccg ccgacatcgg cacagggctt 60
gccgatgcac taactgcgcc gctcgaccat aaagacaaag gtttgaaatc cctgacattg 120
gaagactcca tttcccaaaa cggaacactg accctgtcgg cacaagggtgc ggaaaaaact 180
ttcaaagtgc gcgacaaaga caacagtctc aatacaggca aattgaagaa cgacaaaatc 240
agccgcttcg actttgtgca aaaaatcgaa gtggacggac aaaccatcac gctggcaagc 300
ggcgaatttc aaatatacaa acaggaccac tccgccgtcg ttgccctaca gattgaaaaa 360
atcaacaacc ccgacaaaat cgacagcctg ataaaccaac gtccttctct tgtcagcggc 420
ttggggcggag aacataccgc cttcaaccaa ctgcccagcg gcaaagccga gtatcacggc 480
aaagcattca gtcgcgacga tgccggcgga aaactgacct ataccataga ttttgccgcc 540
aaacagggaac acggcaaaat cgaacacctg aaaacacccg agcagaatgt cgagcttgcc 600
tccgccgaac tcaaagcaga tgaaaaatca cagcccgta ttttgggcga cacgcgctac 660
ggcagcgaag aaaaaggcac ttaccacctc gctcttttcg gcgaccgagc ccaagaaatc 720
gccggctcgg caaccgtgaa gataagggaa aagggttcacg aaatcggcac cgccggcaaa 780
cagtag 786

<210> 54
<211> 261
<212> PRT
<213> *Neisseria meningitidis*

<400> 54

Met Ser Ser Gly Ser Gly Ser Gly Gly Gly Gly Val Ala Ala Asp Ile
1 5 10 15

Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp
20 25 30

Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn Gly
35 40 45

50

Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Val Gly
 50 55 60

Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile
 65 70 75 80

Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr Ile
 85 90 95

Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser Ala
 100 105 110

Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp
 115 120 125

Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly Glu
 130 135 140

His Thr Ala Phe Asn Gln Leu Pro Ser Gly Lys Ala Glu Tyr His Gly
 145 150 155 160

Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile
 165 170 175

Asp Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr
 180 185 190

Pro Glu Gln Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu
 195 200 205

Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu
 210 215 220

Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile
 225 230 235 240

Ala Gly Ser Ala Thr Val Lys Ile Arg Glu Lys Val His Glu Ile Gly
 245 250 255

Ile Ala Gly Lys Gln
 260

<210> 55
 <211> 786
 <212> DNA
 <213> *Neisseria meningitidis*

<400> 55
 tgcagcagcg gaagcggaag cggaggcggc ggtgtcgccg ccgacatcgg cacagggctt 60
 gccgatgcac taactgcgcc gctcgaccat aaagacaaag gtttgaaatc cctgacattg 120
 gaagactcca tttcccaaaa cggaacactg accctgtcgg cacaagggtgc ggaaaaaact 180
 ttcaaagtcg gcgacaaaga caacagtctc aatacaggca aattgaagaa cgacaaaatc 240
 agccgcttcg actttgtgca aaaaatcgaa gtggacggac aaaccatcac gctggcaagc 300
 ggcgaaatttc aaatatacaa acaggaccac tccgccgtcg ttgccctaca gattgaaaaa 360
 atcaacaacc ccgacaaaat cgacagcctg ataaaccaac gctccttcct tgtcagcggc 420
 ttggggcggag aacataccgc cttcaaccaa ctgcccgagc gcaaagccga gtatcacggc 480
 aaagcattca gctccgacga tgccggcgga aaactgacct ataccataga ttttgccgcc 540
 aaacagggac acggcaaaat cgaacacctg aaaacacccg agcagaatgt cgagcttgcc 600
 tccgccgaac tcaaagcaga tgaaaaatca cagcccgta ttttgggcga cagcgctac 660
 ggcagcgaag aaaaaggcac ttaccacctc gctcttttcg gcgaccgagc ccaagaaatc 720
 gccggctcgg caaccgtgaa gataagggaa aaggttcacg aaatcggcat cgccggcaaa 780
 cagtag 786

<210> 56
 <211> 261
 <212> PRT
 <213> *Neisseria meningitidis*

<400> 56

Cys Ser Ser Gly Ser Gly Ser Gly Gly Gly Gly Val Ala Ala Asp Ile
 1 5 10 15

Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp
 20 25 30

Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn Gly
 35 40 45

Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Val Gly
 50 55 60

52

Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile
 65 70 75 80

Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr Ile
 85 90 95

Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser Ala
 100 105 110

Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp
 115 120 125

Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly Glu
 130 135 140

His Thr Ala Phe Asn Gln Leu Pro Ser Gly Lys Ala Glu Tyr His Gly
 145 150 155 160

Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile
 165 170 175

Asp Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr
 180 185 190

Pro Glu Gln Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu
 195 200 205

Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu
 210 215 220

Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile
 225 230 235 240

Ala Gly Ser Ala Thr Val Lys Ile Arg Glu Lys Val His Glu Ile Gly
 245 250 255

Ile Ala Gly Lys Gln
 260

<210> 57

<211> 789

<212> DNA

<213> Neisseria meningitidis

<400> 57
 tgcggatcca gcggaagcgg aagcggaggg ggcggtgtcg ccgccgacat cggcacaggg 60
 cttgccgatg cactaactgc gccgctcgac cataaagaca aaggtttgaa atccctgaca 120
 ttggaagact ccatttccca aaacggaaca ctgacctgt cggcacaagg tgcggaaaaa 180
 actttcaaag tcggcgacaa agacaacagt ctcaatacag gcaaattgaa gaacgacaaa 240
 atcagccgct tcgactttgt gcaaaaaatc gaagtggacg gacaaacct cagctggca 300
 agcggcgaat ttcaaata caaacaggac cactccgccg tcgttgccct acagattgaa 360
 aaaatcaaca accccgacaa aatcgacagc ctgataaacc aacgctcctt ccttgtcagc 420
 ggtttgggcg gagaacatac cgccttcaac caactgcccc gcggcaaagc cgagtatcac 480
 ggcaaagcat tcagctccga cgatgccggc ggaaaactga cctataccat agattttgcc 540
 gccaaacagg gacacggcaa aatcgaacac ctgaaaacac ccgagcagaa tgtcgagctt 600
 gcctccgccg aactcaaagc agatgaaaaa tcacacgccg tcattttggg cgacacgcgc 660
 tacggcagcg aagaaaaagg cacttaccac ctcgctcttt tcggcgaccg agcccaagaa 720
 atcgccggct cggcaaccgt gaagataagg gaaaaggttc acgaaatcgg catcgccggc 780
 aaacagtag 789

<210> 58
 <211> 262
 <212> PRT
 <213> Neisseria meningitidis

<400> 58
 Cys Gly Ser Ser Gly Ser Gly Ser Gly Gly Gly Gly Val Ala Ala Asp
 1 5 10 15
 Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys
 20 25 30
 Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn
 35 40 45
 Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Val
 50 55 60
 Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys
 65 70 75 80

Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr
85 90 95

Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser
100 105 110

Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile
115 120 125

Asp	Ser	Leu	Ile	Asn	Gln	Arg	Ser	Phe	Leu	Val	Ser	Gly	Leu	Gly	Gly
	130					135					140				

Glu His Thr Ala Phe Asn Gln Leu Pro Ser Gly Lys Ala Glu Tyr His
145 150 155 160

Gly Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr
165 170 175

Ile Asp Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys
180 185 190

Thr Pro Glu Gln Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala Asp
195 200 205

Glu Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu
210 215 220

Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu
225 230 235 240

Ile Ala Gly Ser Ala Thr Val Lys Ile Arg Glu Lys Val His Glu Ile
245 250 255

Gly Ile Ala Gly Lys Gln
260

<210> 59

<211> 786

<212> DNA

<213> *Neisseria meningitidis*

<400> 59

atgagcagcg gaagcggaag cggaggcggc ggtgtcgccg ccgacatcgg cacagggctt 60


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gccgatgcac taactgcgcc gctcgaccat aaagacaaaag gtttgaaatc cctgacattg      120
gaagactcca tttcccaaaa cggaacactg accctgtcgg cacaaggtgc ggaaaaaact      180
ttcaaagtgc gcgacaaaaga caacagtctc aatacaggca aattgaagaa cgacaaaatc      240
agccgcttcg actttgtgca aaaaatcgaa gtggacggac aaaccatcac gctggcaagc      300
ggcgaatttc aaatatacaa acaggaccac tccgccgtcg ttgccctaca gattgaaaaa      360
atcaacaacc ccgacaaaat cgacagcctg ataaaccaac gtccttcct tgtcagcggg      420
ttggggcggag aacataccgc cttcaaccaa ctgcccagcg gcaaagccga gtatcacggc      480
aaagcattca gctccgacga tgccggcgga aaactgacct ataccataga ttttgccgcc      540
aaacaggggac acggcaaaaat cgaacacctg aaaacacccg agcagaatgt cgagcttgcc      600
tccgccgaac tcaaagcaga tgaaaaatca cacgccgtca ttttgggcga cacgcgctac      660
ggcagcgaag aaaaaggcac ttaccacctc gctcttttcg gcgaccgagc ccaagaaatc      720
gccggctcgg caaccgtgaa gataagggaa aaggttcacg aaatcggcat cgccggcaaa      780
cagtag                                          786

```

```

<210> 60
<211> 261
<212> PRT
<213> Neisseria meningitidis
<400> 60

```

```

Met Ser Ser Gly Ser Gly Ser Gly Gly Gly Gly Val Ala Ala Asp Ile
1           5           10           15

```

```

Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp
          20           25           30

```

```

Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn Gly
          35           40           45

```

```

Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Val Gly
          50           55           60

```

```

Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile
65           70           75           80

```

```

Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr Ile
          85           90           95

```


Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser Ala
 100 105 110

Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp
 115 120 125

Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly Glu
 130 135 140

His Thr Ala Phe Asn Gln Leu Pro Ser Gly Lys Ala Glu Tyr His Gly
 145 150 155 160

Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile
 165 170 175

Asp Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr
 180 185 190

Pro Glu Gln Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu
 195 200 205

Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu
 210 215 220

Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile
 225 230 235 240

Ala Gly Ser Ala Thr Val Lys Ile Arg Glu Lys Val His Glu Ile Gly
 245 250 255

Ile Ala Gly Lys Gln
 260

<210> 61

<211> 789

<212> DNA

<213> Neisseria meningitidis

<400> 61

tgcagcagcg gaggcggcgg aagcggaggc ggcggtgtcg cgcgcgacat cggcacgggg 60

cttgccgatg cactaactgc gccgctcgac cataaagaca aaggtttgaa atccctgaca 120

ttggaagact ctattcccca aaacggaaca ctaaccctgt cggcacaagg tgcggaaaaa 180


```

actttcaaag ccggcgacaa agacaacagc ctcaacacgg gcaaactgaa gaacgacaaa   240
atcagccgct tcgactttgt gcaaaaaatc gaagtggacg gacaaaccat cacgctggca   300
agcggcgaat ttcaaataa caaacaggac cactccgccc tcgttgccct acagattgaa   360
aaaatcaaca accccgacaa aatcgacagc ctgataaacc aacgctcctt ccttgtcagc   420
ggtttgggcg gagaacatac cgccttcaac caactgcccg gcggcaaagc cgagtatcac   480
ggcaaagcat tcagctccga cgacccgaac ggcaggctgc actactccat tgattttacc   540
aaaaaacagg gttacggcgg aatcgaacac ctgaaaacac ccgagcaaaa tgctcagcctt   600
gcctccgccc aactcaaagc agatgaaaaa tcacacgccg tcattttggg cgacacgcgc   660
tacggcagcg aagaaaaagg cacttaccac ctcgcccttt tcggcgaccg cgcccaagaa   720
atcgccggct cggcaaccgt gaagataggg gaaaagggtt acgaaatcgg catcgccggc   780
aaacagtag                                     789

```

```

<210> 62
<211> 262
<212> PRT
<213> Neisseria meningitidis

```

```

<400> 62

```

```

Cys Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Val Ala Ala Asp
1           5           10           15

```

```

Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys
          20           25           30

```

```

Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Pro Gln Asn
          35           40           45

```

```

Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Ala
          50           55           60

```

```

Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys
65           70           75           80

```

```

Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr
          85           90           95

```

```

Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser
          100          105          110

```


Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile
 115 120 125

Asp Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly
 130 135 140

Glu His Thr Ala Phe Asn Gln Leu Pro Gly Gly Lys Ala Glu Tyr His
 145 150 155 160

Gly Lys Ala Phe Ser Ser Asp Asp Pro Asn Gly Arg Leu His Tyr Ser
 165 170 175

Ile Asp Phe Thr Lys Lys Gln Gly Tyr Gly Gly Ile Glu His Leu Lys
 180 185 190

Thr Pro Glu Gln Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala Asp
 195 200 205

Glu Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu
 210 215 220

Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu
 225 230 235 240

Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Glu Ile
 245 250 255

Gly Ile Ala Gly Lys Gln
 260

<210> 63
 <211> 792
 <212> DNA
 <213> Neisseria meningitidis

<400> 63
 tgcggatcca gcggaggcgg cggaagcgga ggcggcggtg tcgccgccga catcggcacg 60
 gggcttgccg atgcactaac tgcgccgctc gaccataaag acaaaggttt gaaatccctg 120
 acattggaag actctattcc ccaaaacgga aactaacc tgcggcaca aggtgcggaa 180
 aaaactttca aagccggcga caaagacaac agcctcaaca cgggcaaact gaagaacgac 240
 aaaatcagcc gcttcgactt tgtgcaaaaa atcgaagtgg acggacaaac catcacgctg 300

59

```

gcaagcggcg aatttcaa atacaaacag gaccactccg ccgtcgttgc cctacagatt 360
gaaaaaatca acaaccccg caaaatcgac agcctgataa accaacgctc cttccttgtc 420
agcggtttgg gcggagaaca taccgccttc aaccaactgc ccggcggcaa agccgagtat 480
cacggcaaag cattcagctc cgacgacccg aacggcaggc tgcactactc cattgatttt 540
acaaaaaac agggttacgg cggaatcgaa cacctgaaaa cacccgagca aaatgtcgag 600
cttgctccg ccgaactcaa agcagatgaa aaatcacacg ccgtcatttt gggcgacacg 660
cgctacggca gcgaagaaaa aggcacttac cacctcgccc ttttcggcga ccgcgccc 720
gaaatcgccg gctcggcaac cgtgaagata ggggaaaagg ttcacgaaat cggcatcgcc 780
ggcaaacagt ag 792

```

```

<210> 64
<211> 263
<212> PRT
<213> Neisseria meningitidis

<400> 64

```

```

Cys Gly Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Val Ala Ala
1           5           10           15

```

```

Asp Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His
          20           25           30

```

```

Lys Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Pro Gln
35           40           45

```

```

Asn Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys
50           55           60

```

```

Ala Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
65           70           75           80

```

```

Lys Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln
85           90           95

```

```

Thr Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His
100          105          110

```

```

Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys
115          120          125

```


60

Ile Asp Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly
 130 135 140

Gly Glu His Thr Ala Phe Asn Gln Leu Pro Gly Gly Lys Ala Glu Tyr
 145 150 155 160

His Gly Lys Ala Phe Ser Ser Asp Asp Pro Asn Gly Arg Leu His Tyr
 165 170 175

Ser Ile Asp Phe Thr Lys Lys Gln Gly Tyr Gly Gly Ile Glu His Leu
 180 185 190

Lys Thr Pro Glu Gln Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala
 195 200 205

Asp Glu Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser
 210 215 220

Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln
 225 230 235 240

Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Glu
 245 250 255

Ile Gly Ile Ala Gly Lys Gln
 260

<210> 65

<211> 789

<212> DNA

<213> Neisseria meningitidis

<400> 65

atgagcagcg gaggcggcgg aagcggaggc ggcggtgtcg ccgccgacat cggcacgggg 60
 cttgccgatg cactaactgc gccgctcgac cataaagaca aaggtttgaa atccctgaca 120
 ttggaagact ctattcccca aaacggaaca ctaaccctgt cggcacaagg tgcggaaaaa 180
 acttttcaaag ccggcgacaa agacaacagc ctcaacacgg gcaaactgaa gaacgacaaa 240
 atcagccgct tcgactttgt gcaaaaaatc gaagtggacg gacaaaccat cacgctggca 300
 agcggcgaat ttcaaata caaacaggac cactccgccg tcgttgccct acagattgaa 360
 aaaatcaaca accccgacaa aatcgacagc ctgataaacc aacgctcctt ccttgtcagc 420

61

```

ggtttgggcg gagaacatac cgccttcaac caactgcccg gcggcaaagc cgagtatcac    480
ggcaaagcat tcagctccga cgacccgaac ggcaggctgc actactccat tgattttacc    540
aaaaaacagg gttacggcgg aatcgaacac ctgaaaacac ccgagcaaaa tgtcgagctt    600
gcctccgccg aactcaaagc agatgaaaaa tcacacgccg tcattttggg cgacacgcgc    660
tacggcagcg aagaaaaagg cacttaccac ctgcgccctt tcggcgaccg cgcccaagaa    720
atcgccggct cggcaaccgt gaagataggg gaaaaggttc acgaaatcgg catcgccggc    780
aaacagtag                                         789

```

```

<210> 66
<211> 262
<212> PRT
<213> Neisseria meningitidis

```

```

<400> 66

```

```

Met Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Val Ala Ala Asp
1           5           10          15

```

```

Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys
          20          25          30

```

```

Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Pro Gln Asn
          35          40          45

```

```

Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Ala
          50          55          60

```

```

Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys
65          70          75          80

```

```

Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr
          85          90          95

```

```

Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser
          100         105         110

```

```

Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile
          115         120         125

```

```

Asp Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly
          130         135         140

```


Glu His Thr Ala Phe Asn Gln Leu Pro Gly Gly Lys Ala Glu Tyr His
 145 150 155 160

Gly Lys Ala Phe Ser Ser Asp Asp Pro Asn Gly Arg Leu His Tyr Ser
 165 170 175

Ile Asp Phe Thr Lys Lys Gln Gly Tyr Gly Gly Ile Glu His Leu Lys
 180 185 190

Thr Pro Glu Gln Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala Asp
 195 200 205

Glu Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu
 210 215 220

Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu
 225 230 235 240

Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Glu Ile
 245 250 255

Gly Ile Ala Gly Lys Gln
 260

<210> 67
 <211> 774
 <212> DNA
 <213> Neisseria meningitidis

<400> 67
 tgcagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggccttgc cgatgcacta 60
 accgcaccgc tcgaccataa agacaaaggt ttgaaatccc tgacattgga agactccatt 120
 tcccaaaacg gaacactgac cctgtcggca caaggtgcgg aaaaaacttt caaagtcggc 180
 gacaaagaca acagtctcaa tacaggcaaa ttgaagaacg acaaaatcag ccgcttcgac 240
 tttgtgcaaa aaatcgaagt ggacggacaa accatcacgc tggcaagcgg cgaatttcaa 300
 atatacaaac agaaccactc cgccgtcggt gccctacaga ttgaaaaaat caacaacccc 360
 gacaaaatcg acagcctgat aaaccaacgc tccttccttg tcagcgggtt gggcggagaa 420
 cataccgcct tcaaccaact gcccggcggc aaagccgagt atcacggcaa agcattcagc 480
 tccgacgatg ccggcgga aa actgacctat accatagatt ttgccgcaa acagggacac 540

ggcaaaatcg aacacctgaa aacacccgag caaaatgtcg agcttgccgc cgccgaactc 600
 aaagcagatg aaaaatcaca cgccgtcatt ttgggcgaca cgcgctacgg cagcgaagaa 660
 aaaggcactt accacctcgc ccttttcggc gaccgcgctc aagaaatcgc cggctcggca 720
 accgtgaaga taggagaaaa gggttcacgaa atcagcatcg ccggcaaaca gtag 774

<210> 68
 <211> 257
 <212> PRT
 <213> Neisseria meningitidis

<400> 68

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Lys
 20 25 30

Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn Gly Thr Leu Thr Leu
 35 40 45

Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Val Gly Asp Lys Asp Asn
 50 55 60

Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile Ser Arg Phe Asp
 65 70 75 80

Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr Ile Thr Leu Ala Ser
 85 90 95

Gly Glu Phe Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val Ala Leu
 100 105 110

Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn
 115 120 125

Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe
 130 135 140

Asn Gln Leu Pro Gly Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser
 145 150 155 160

Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala

64

	165		170		175
Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn					
	180		185		190
Val Glu Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala					
	195		200		205
Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr					
	210		215		220
His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala					
	225		230		235
					240
Thr Val Lys Ile Gly Glu Lys Val His Glu Ile Ser Ile Ala Gly Lys					
	245		250		255

Gln

<210> 69

<211> 777

<212> DNA

<213> Neisseria meningitidis

<400> 69

tgcggatcca gcgaggcg cggtgtcgcc gccgacatcg gcgcggggct tgccgatgca	60
ctaaccgcac cgctcgacca taaagacaaa ggtttgaaat ccctgacatt ggaagactcc	120
atttcccaaa acggaacact gaccctgtcg gcacaagggtg cggaaaaaac tttcaaagtc	180
ggcgacaaaag acaacagtct caatacaggc aaattgaaga acgacaaaat cagccgcttc	240
gactttgtgc aaaaaatcga agtggacgga caaaccatca cgctggcaag cggcgaattt	300
caaataataca aacagaacca ctccgccgtc gttgccttac agattgaaaa aatcaacaac	360
cccgacaaaa tcgacagcct gataaaccaa cgctccttcc ttgtcagcgg tttgggcgga	420
gaacataccg ctttcaacca actgcccggc ggcaaagccg agtatcacgg caaagcattc	480
agctccgacg atgccggcgg aaaactgacc tataccatag attttgccgc caaacaggga	540
cacggcaaaa tcgaacacct gaaaacaccc gagcaaaatg tcgagcttgc cgccgccgaa	600
ctcaaagcag atgaaaaatc acacgccgtc attttgggcg acacgcgcta cggcagcgaa	660
gaaaaaggca cttaccacct cgcccttttc ggcgaccgcg ctcaagaaat cgccggctcg	720

65

gcaaccgtga agataggaga aaaggttcac gaaatcagca tcgccggcaa acagtag 777

<210> 70

<211> 258

<212> PRT

<213> Neisseria meningitidis

<400> 70

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu
 20 25 30

Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn Gly Thr Leu Thr
 35 40 45

Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Val Gly Asp Lys Asp
 50 55 60

Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile Ser Arg Phe
 65 70 75 80

Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr Ile Thr Leu Ala
 85 90 95

Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val Ala
 100 105 110

Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile
 115 120 125

Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala
 130 135 140

Phe Asn Gln Leu Pro Gly Gly Lys Ala Glu Tyr His Gly Lys Ala Phe
 145 150 155 160

Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala
 165 170 175

Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln
 180 185 190

Asn Val Glu Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His
 195 200 205

Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr
 210 215 220

Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser
 225 230 235 240

Ala Thr Val Lys Ile Gly Glu Lys Val His Glu Ile Ser Ile Ala Gly
 245 250 255

Lys Gln

<210> 71
 <211> 774
 <212> DNA
 <213> Neisseria meningitidis

<400> 71
 atgagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggccttgc cgatgcacta 60
 accgcaccgc tcgaccataa agacaaaggt ttgaaatccc tgacattgga agactccatt 120
 tcccaaaacg gaacactgac cctgtcggca caaggtgcgg aaaaaacttt caaagtcggc 180
 gacaaagaca acagtctcaa tacaggcaaa ttgaagaacg aaaaaatcag ccgcttcgac 240
 tttgtgcaaa aaatcgaagt ggacggacaa accatcacgc tggcaagcgg cgaatttcaa 300
 atatacaaac agaaccactc cgccgtcggt gccctacaga ttgaaaaaat caacaacccc 360
 gacaaaaatcg acagcctgat aaaccaacgc tccttccttg tcagcgggttt gggcggagaa 420
 cataccgcct tcaaccaact gcccggcggc aaagccgagt atcacggcaa agcattcagc 480
 tccgacgatg ccggcggaaa actgacctat accatagatt ttgccgcaa acagggacac 540
 ggcaaaatcg aacacctgaa aacacccgag caaaatgtcg agcttgccgc cgccgaactc 600
 aaagcagatg aaaaaatcaca cgccgtcatt ttgggcgaca cgcgctacgg cagcgaagaa 660
 aaaggcactt accacctcgc ccttttcggc gaccgcgctc aagaaatcgc cggctcggca 720
 accgtgaaga taggagaaaa gggtcacgaa atcagcatcg ccggcaaaca gtag 774

<210> 72
 <211> 257
 <212> PRT

<213> Neisseria meningitidis

<400> 72

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Lys
 20 25 30

Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn Gly Thr Leu Thr Leu
 35 40 45

Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Val Gly Asp Lys Asp Asn
 50 55 60

Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile Ser Arg Phe Asp
 65 70 75 80

Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr Ile Thr Leu Ala Ser
 85 90 95

Gly Glu Phe Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val Ala Leu
 100 105 110

Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn
 115 120 125

Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe
 130 135 140

Asn Gln Leu Pro Gly Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser
 145 150 155 160

Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala
 165 170 175

Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn
 180 185 190

Val Glu Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala
 195 200 205

Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr

68

210	215	220
His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala		
225	230	235 240
Thr Val Lys Ile Gly Glu Lys Val His Glu Ile Ser Ile Ala Gly Lys		
	245	250 255

Gln

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<210> 73
<211> 765
<212> DNA
<213> Neisseria meningitidis

<400> 73
tgcagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta 60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc 120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc 180
gacagcctca atacgggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt 240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa 300
caggaccact ccgccgtcgt tgccttacag attgaaaaaa tcaacaaccc cgacaaaatc 360
gacagcctga taaaccaacg ctccttcctt gtcagcgggt tgggtggaga acataccgcc 420
ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgat 480
gctggcggaa aactgaccta taccatagat ttcgccgcca aacagggaca cggcaaaatc 540
gaacacttga aaacaccgga gcaaaatgtc gagcttgctt ccgccgaact caaagcagat 600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact 660
taccacctcg cccttctcgg cgaccgcgcc caagaaatcg cgggctcggc aaccgtgaag 720
ataagggaaa aggttcacga aatcggcatt gccggcaaac agtag 765

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<210> 74
<211> 254
<212> PRT
<213> Neisseria meningitidis

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<400> 74

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Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Leu Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
245 250

<210> 75

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 75

tgcggatcca	gcggaggcgg	cggtgtcgcc	gccgacatcg	gcgcgggggct	tgccgatgca	60
ctaaccgcac	cgctcgacca	taaagacaaa	agtttgcagt	ctttgacgct	ggatcagtc	120
gtcaggaaaa	acgagaaact	gaagctggcg	gcacaagggtg	cggaaaaaac	ttatggaaac	180
ggcgacagcc	tcaatacggg	caaattgaag	aacgacaagg	tcagccgctt	cgactttatc	240
cgtcaaatac	aagtggacgg	gcagctcatt	accttggaga	gcggagaggtt	ccaaatatac	300
aaacaggacc	actccgccgt	cgttgcccta	cagattgaaa	aatcaacaa	ccccgacaaa	360
atcgacagcc	tgataaacca	acgctccttc	cttgtcagcg	gtttgggtgg	agaacatacc	420
gccttcaacc	aactgcccag	cggcaaagcc	gagtatcacg	gcaaagcatt	cagctccgac	480
gatgctggcg	gaaaactgac	ctataccata	gatttgcgcg	ccaaacaggg	acacggcaaa	540
atcgaacact	tgaaaacacc	cgagcaaaat	gtcgagcttg	cctccgccga	actcaaagca	600
gatgaaaaat	cacacgccgt	cattttgggc	gacacgcgct	acggcggcga	agaaaaaggc	660
acttaccacc	tcgcccttct	cggcgaccgc	gcccaagaaa	tcgccggctc	ggcaaccgtg	720
aagataaggg	aaaagggttc	cgaaatcggc	attgccggca	aacagtag		768

<210> 76

<211> 255

<212> PRT

<213> Neisseria meningitidis

<400> 76

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
35 40 45

71

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
 85 90 95

Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile
 100 105 110

Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
 115 120 125

Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln
 130 135 140

Leu Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu
 180 185 190

Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile
 195 200 205

Leu Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu
 210 215 220

Ala Leu Leu Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val
 225 230 235 240

Lys Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250 255

<210> 77

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 77
 atgagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta 60
 accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc 120
 agggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc 180
 gacagcctca atacgggcaa attgaagaac gacaagggtca gccgcttcga ctttatccgt 240
 caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa 300
 caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc 360
 gacagcctga taaaccaacg ctccttcctt gtcagcggtt tgggtggaga acataccgcc 420
 ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgat 480
 gctggcggaa aactgaccta taccatagat ttgccgccca aacagggaca cggcaaaatc 540
 gaacacttga aaacacccga gcaaaatgtc gagcttgcct ccgccgaact caaagcagat 600
 gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact 660
 taccacctcg cccttctcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag 720
 ataagggaaa aggttcacga aatcggcatt gccggcaaac agtag 765

<210> 78
 <211> 254
 <212> PRT
 <213> Neisseria meningitidis

<400> 78

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Leu Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 79

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 79

tgcagcagcg gaggcggcgg tgcgcgccg gacatcggcg cggggccttgc cgatgcacta	60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcctgc	120
aggaaaaacg agaaactgaa gctggcggca caagggtgcgg aaaaaactta tggaaacggc	180
gacagcctca atacgggcaa attgaagaac gacaagggtca gccgcttcga ctttatccgt	240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa	300


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caggaccact ccgccgtcgt tgcctacag attgaaaaaa tcaacaaccc cgacaaaatc 360
gacagcctga taaaccaacg ctccctcctt gtcagcgggt tgggtggaga acataccgcc 420
ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgat 480
gctggcgga aactgacctt taccatagat ttccgcgcca aacagggaca cggcaaaatc 540
gaacacttga aaacacccga gcaaaatgtc gagcttgctt ccgccgaact caaagcagat 600
gaaaaatcac acgcgcgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact 660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag 720
ataagggaag aggttcacga aatcggcatc gccggcaaac agtag 765

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<210> 80
<211> 254
<212> PRT
<213> Neisseria meningitidis

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<400> 80

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Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10           15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
          20           25           30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35           40           45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50           55           60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65           70           75           80

```

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Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
          85           90           95

```

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Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
          100          105          110

```

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Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
          115          120          125

```


Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 81

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 81

tgcggatcca gcggaggcgg cgggtgtcgcc gccgacatcg gcgcgggggct tgccgatgca	60
ctaaccgcac cgctcgacca taaagacaaa agtttgcagt ctttgacgct ggatcagtc	120
gtcaggaaaa acgagaaact gaagctggcg gcacaagggt cggaaaaaac ttatggaaac	180
ggcgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgctt cgactttatc	240
cgtcaaactc aagtggacgg gcagctcatt accttgagga gcggagagtt ccaaataac	300
aaacaggacc actccgccgt cgttgcccta cagattgaaa aatcaacaa ccccgacaaa	360
atcgacagcc tgataaacca acgctccttc cttgtcagcg gtttgggtgg agaacatacc	420
gccttcaacc aactgcccag cggcaaagcc gaggatcacg gcaaagcatt cagctccgac	480
gatgctggcg gaaaactgac ctataccata gatttcgccg ccaaacaggg acacggcaaa	540
atcgaacact tgaaaacacc cgagcaaaat gtcgagcttg cctccgccga actcaaagca	600

gatgaaaaat cacacgccgt cattttgggc gacacgcgct acggcggcga agaaaaaggc 660
 acttaccacc tcgccctttt cggcgaccgc gcccaagaaa tcgccggctc ggcaaccgtg 720
 aagataaggg aaaaggttca cgaaatcggc atcgccggca aacagtag 768

<210> 82
 <211> 255
 <212> PRT
 <213> Neisseria meningitidis

<400> 82

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
 20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
 35 40 45

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
 85 90 95

Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile
 100 105 110

Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
 115 120 125

Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln
 130 135 140

Leu Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu
 180 185 190

Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile
 195 200 205

Leu Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu
 210 215 220

Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val
 225 230 235 240

Lys Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250 255

<210> 83

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 83

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atgagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcgcgc      120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc      180
gacagcctca atacgggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt      240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa      300
caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc      360
gacagcctga taaaccaacg ctcttctctt gtcagcgggt tgggtggaga acataccgcc      420
ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgat      480
gctggcggaa aactgaccta taccatagat ttcgccgcc aacagggaca cggcaaaatc      540
gaacacttga aaacacccga gcaaaatgtc gagcttgcct ccgccgaact caaagcagat      600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact      660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag      720
ataagggaaa aggttcacga aatcggcatc gccggcaaac agtag                          765

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<210> 84

<211> 254

78

<212> PRT

<213> *Neisseria meningitidis*

<400> 84

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

79

Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 85

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 85

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tgcagcagcg gagggcgcg tgtcgccgcc gacatcggcg cggggccttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc      120
aggaaaaacg agaaactgaa gctggcgggca caaggtgcgg aaaaaactta tggaaacggc      180
gacagcctca atacggggcaa attgaagaac gacaagggtca gccgcttcga ctttatccgt      240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa      300
caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc      360
gacagcctga taaaccaacg ctccctcctt gtcagcgggt tgggtggaga acataccgcc      420
ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgat      480
gctggcgga aactgaccta taccatagat ttcgccgcc aacagggaca cggcaaaatc      540
gaacacttga aaacacccga gcaaaatgtc gagcttgcct ccgccgaact caaagcagat      600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact      660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag      720
ataagggaag aggttcacga aatcggcatc gccggcaaac agtag                          765

```

<210> 86

<211> 254

<212> PRT

<213> Neisseria meningitidis

<400> 86

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln

80

20	25	30
Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu		
35	40	45
Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn		
50	55	60
Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg		
65	70	75
Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe		
85	90	95
Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu		
100	105	110
Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser		
115	120	125
Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu		
130	135	140
Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp		
145	150	155
Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly		
165	170	175
His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu		
180	185	190
Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu		
195	200	205
Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala		
210	215	220
Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys		
225	230	235
Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln		
245	250	

<210> 87
 <211> 768
 <212> DNA
 <213> *Neisseria meningitidis*

<400> 87
 tgcggatcca gcggaggcgg cgggtgtcgcc gccgacatcg gcgcggggct tgccgatgca 60
 ctaaccgcac cgctcgacca taaagacaaa agtttgcagt ctttgacgct ggatcagtcc 120
 gtcaggaaaa acgagaaact gaagctggcg gcacaagggtg cggaaaaaac ttatggaaac 180
 ggcgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgctt cgactttatc 240
 cgtcaaatcg aagtggacgg gcagctcatt accttggaga gcggagagtt ccaaataac 300
 aaacaggacc actccgccgt cgttgcccta cagattgaaa aaatcaacaa ccccgacaaa 360
 atcgacagcc tgataaacca acgctccttc cttgtcagcg gtttgggtgg agaacatacc 420
 gccttcaacc aactgcccag cggcaaagcc gagtatcacg gcaaagcatt cagctccgac 480
 gatgctggcg gaaaactgac ctataccata gatttcgccg ccaaacaggg acacggcaaa 540
 atcgaacact tgaaaacacc cgagcaaaat gtcgagcttg cctccgccga actcaaagca 600
 gatgaaaaat cacacgccgt cattttgggc gacacgcgct acggcggcga agaaaaaggc 660
 acttaccacc tcgccctttt cggcgaccgc gcccaagaaa tcgccggctc ggcaaccgtg 720
 aagataaggg aaaaggttca cgaaatcggc atcgccggca aacagtag 768

<210> 88
 <211> 255
 <212> PRT
 <213> *Neisseria meningitidis*

<400> 88

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
 20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
 35 40 45

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60

82

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
65 70 75 80

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
85 90 95

Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile
100 105 110

Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
115 120 125

Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln
130 135 140

Leu Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp
145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu
180 185 190

Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile
195 200 205

Leu Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu
210 215 220

Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val
225 230 235 240

Lys Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
245 250 255

<210> 89

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 89

atgagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta 60


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accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc 120
aggaaaaacg agaaactgaa gctggcggca caaggtgctg aaaaaactta tggaaacggc 180
gacagcctca atacgggcaa attgaagaac gacaagggtca gccgcttoga ctttatccgt 240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa 300
caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc 360
gacagcctga taaaccaacg ctcccttctt gtcagcgggt tgggtggaga acataccgcc 420
ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgat 480
gctggcggaa aactgaccta taccatagat ttccgcgcc aacagggaca cggcaaaatc 540
gaacacttga aaacacccga gcaaaatgtc gagcttgctt ccgccgaact caaagcagat 600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact 660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag 720
ataagggaaa aggttcacga aatcggcatc gccggcaaac agtag 765

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<210> 90
<211> 254
<212> PRT
<213> Neisseria meningitidis

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```

<400> 90

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```

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10           15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
           20           25           30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
           35           40           45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
           50           55           60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65           70           75           80

```

```

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
           85           90           95

```

```

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu

```


100	105	110
Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser		
115	120	125
Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu		
130	135	140
Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp		
145	150	155
Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly		
165	170	175
His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu		
180	185	190
Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu		
195	200	205
Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala		
210	215	220
Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys		
225	230	235
Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln		
245	250	

<210> 91

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 91

tgcagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta 60

accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcgcgc 120

aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc 180

gacagcctca atacgggcaa attgaagaac gacaaggcca gccgcttcga ctttatccgt 240

caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa 300

caggaccact ccgccgtcgt tgccttacag attgaaaaaa tcaacaaccc cgacaaaatc 360


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gacagcctga taaaccaacg ctcttcctt gtcagcgggt tgggtggaga acataccgcc 420
ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgat 480
gctggcgga aactgaccta taccatagat ttcgccgcca aacagggaca cggcaaaatc 540
gaacacttga aaacacccga gcaaaatgtc gagcttgctt ccgccgaact caaagcagat 600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact 660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag 720
ataagggaaa aggttcacga aatcggcatc gccggcaaac agtag 765

```

```

<210> 92
<211> 254
<212> PRT
<213> Neisseria meningitidis

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```

<400> 92

```

```

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10           15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
          20           25           30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35           40           45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50           55           60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65           70           75           80

```

```

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
          85           90           95

```

```

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
          100          105          110

```

```

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
          115          120          125

```

```

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
          130          135          140

```


Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 93
 <211> 768
 <212> DNA
 <213> Neisseria meningitidis

<400> 93
 tgcggatcca gcggaggcgg cgggtgtcgcc gccgacatcg gcgcgggggct tgccgatgca 60
 ctaaccgcac cgctcgacca taaagacaaa agtttgcagt ctttgacgct ggatcagtc 120
 gtcaggaaaa acgagaaaact gaagctggcg gcacaagggtg cggaaaaaac ttatggaaac 180
 ggcgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgctt cgactttatc 240
 cgtcaaactcg aagtggacgg gcagctcatt accttgagaga gcggagagtt ccaaataac 300
 aaacaggacc actccgccgt cgttgcccta cagattgaaa aaatcaacaa ccccgacaaa 360
 atcgacagcc tgataaacca acgctccttc cttgtcagcg gtttgggtgg agaacatacc 420
 gccttcaacc aactgcccag cggcaaagcc gagtatcacg gcaaagcatt cagctccgac 480
 gatgctggcg gaaaactgac ctataccata gatttcgccg ccaaacaggg acacggcaaa 540
 atcgaacact tgaaaacacc cgagcaaaat gtcgagcttg cctccgccga actcaaagca 600
 gatgaaaaat cacacgccgt cattttgggc gacacgcgct acggcgccga agaaaaaggc 660

acttaccacc tcgccctttt cggcgaccgc gcccaagaaa tcgccggctc ggcaaccgtg 720

aagataaggg aaaaggttca cgaaatcggc atcgccggca aacagtag 768

<210> 94

<211> 255

<212> PRT

<213> Neisseria meningitidis

<400> 94

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
35 40 45

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
50 55 60

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
65 70 75 80

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
85 90 95

Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile
100 105 110

Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
115 120 125

Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln
130 135 140

Leu Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp
145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu

88

180	185	190
Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile		
195	200	205
Leu Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu		
210	215	220
Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val		
225	230	235 240
Lys Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln		
245	250	255

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<210> 95
<211> 765
<212> DNA
<213> Neisseria meningitidis

<400> 95
atgagcagcg gagggcgcg tgctcgccgcc gacatcggcg cggggcttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc      120
aggaaaaacg agaaactgaa gctggcgggca caaggtgcgg aaaaaactta tggaaacggc      180
gacagcctca atacgggcaa attgaagaac gacaaggcca gccgcttcga ctttatccgt      240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa      300
caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc      360
gacagcctga taaaccaacg ctccctcctt gtcagcggtt tgggtggaga acataccgcc      420
ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgat      480
gctggcgga aactgaccta taccatagat ttcgccgcca aacagggaca cggcaaaatc      540
gaacacttga aaacacccga gcaaaatgtc gagcttgcct ccgccgaact caaagcagat      600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact      660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag      720
ataagggaaa aggttcacga aatcggcatc gccggcgaac agtag                          765

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<210> 96
<211> 254
<212> PRT
<213> Neisseria meningitidis

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<400> 96

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

90

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 97

<211> 765

<212> DNA

<213> *Neisseria meningitidis*

<400> 97

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tgcagcagcg gaggcggcgg tgtcgccgcc gacatcgggc cggggccttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcgcgc      120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc      180
gacagcctca atacgggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt      240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa      300
caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc      360
gacagcctga taaaccaacg ctccttcctt gtcagcgggt tgggtggaga acataccgcc      420
ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgat      480
gctggcggaa aactgaccta taccatagat ttcgccgcca aacagggaca cggcaaaatc      540
gaacacttga aaacacccga gcaaaatgtc gagcttgccct ccgccgaact caaagcagat      600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact      660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag      720
ataagggaaa aggttcacga aatcggcacg gccggcaaac agtaa                        765

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<210> 98

<211> 254

<212> PRT

<213> *Neisseria meningitidis*

<400> 98

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45
 Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60
 Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80
 Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95
 Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110
 Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125
 Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140
 Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160
 Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175
 His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190
 Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205
 Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220
 Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240
 Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<211> 768
 <212> DNA
 <213> *Neisseria meningitidis*

<400> 99
 tgcggatcca gcgaggcgg cgggtgtcgcc gccgacatcg gcgcgggggct tgccgatgca 60
 ctaaccgcac cgctcgacca taaagacaaa agtttgcagt ctttgacgct ggatcagtcc 120
 gtcaggaaaa acgagaaact gaagctggcg gcacaagggtg cggaaaaaac ttatggaaac 180
 ggcgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgctt cgactttatc 240
 cgtcaaatcg aagtggacgg gcagctcatt accttggaaga gcggagagtt ccaaataatac 300
 aaacaggacc actccgccgt cgttgcccta cagattgaaa aaatcaacaa ccccgacaaa 360
 atcgacagcc tgataaacca acgctccttc cttgtcagcg gtttgggtgg agaacatacc 420
 gccttcaacc aactgccag cggcaaagcc gagtatcacg gcaaagcatt cagctccgac 480
 gatgctggcg gaaaactgac ctataccata gatttcgccg ccaaacagggt acacggcaaa 540
 atcgaacact tgaaaacacc cgagcaaaat gtcgagcttg cctccgccga actcaaagca 600
 gatgaaaaat cacacgccgt cattttgggc gacacgcgct acggcggcga agaaaaaggc 660
 acttaccacc tcgccctttt cggcgaccgc gcccaagaaa tcgccggctc ggcaaccgtg 720
 aagataagggt aaaaggttca cgaaatcggc atcgccggca aacagtaa 768

<210> 100
 <211> 255
 <212> PRT
 <213> *Neisseria meningitidis*

<400> 100

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
 20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
 35 40 45

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
85 90 95

Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile
100 105 110

Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
115 120 125

Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln
130 135 140

Leu Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp
145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu
180 185 190

Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile
195 200 205

Leu Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu
210 215 220

Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val
225 230 235 240

Lys Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
245 250 255

<210> 101

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 101

atgagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta 60

accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcgcgc 120

aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaacggc 180

gacagcctca atacgggcaa attgaagaac gacaagggtca gccgcttcga ctttatccgt 240
 caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa 300
 caggaccact ccgccgtcgt tgccttacag attgaaaaaa tcaacaaccc cgacaaaatc 360
 gacagcctga taaaccaacg ctcttctctt gtcagcgggtt tgggtggaga acataccgcc 420
 ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgat 480
 gctggcggaa aactgacctt taccatagat ttgcgcgcca aacagggaca cggcaaaatc 540
 gaacacttga aaacacccga gcaaaatgtc gagcttgcct ccgccgaact caaagcagat 600
 gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact 660
 taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag 720
 ataagggaaa aggttcacga aatcggcatc gccggcaaac agtaa 765

<210> 102

<211> 254

<212> PRT

<213> Neisseria meningitidis

<400> 102

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 103

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 103

tgcagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta	60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc	120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc	180
gacagcctta atacgggcaa attgaagaac gacaaggtca gccgtttcga ctttatccgt	240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa	300
caggaccact ccgccgtcgt tgcctacag attgaaaaaa tcaacaaccc cgacaaaatc	360
gacagcctga taaaccaacg ctccttcctt gtcagcgggt tgggtggaga acataccgcc	420
ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgat	480


```

gctggcgga aactgacct taccatagat ttgcgcgcca aacagggaca cggcaaaatc 540
gaacacttga aaacacccga gcaaaatgtc gagcttgcct ccgccgaact caaagcagat 600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcggaaga aaaaggcact 660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag 720
ataagggaaa aggttcacga aatcggcatc gccggcaaac agtag 765

```

```

<210> 104
<211> 254
<212> PRT
<213> Neisseria meningitidis

```

```

<400> 104

```

```

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10           15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
          20           25           30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35           40           45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50           55           60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65           70           75           80

```

```

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
          85           90           95

```

```

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
          100          105          110

```

```

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
          115          120          125

```

```

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
          130          135          140

```

```

Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
145          150          155          160

```


Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 105

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 105

tgcggatcca gcggaggcgg cgggtgtcgcc gccgacatcg gcgcggggct tgccgatgca	60
ctaaccgcac cgctcgacca taaagacaaa agtttgacgt ctttgacgct ggatcagtcc	120
gtcaggaaaa acgagaaact gaagctggcg gcacaagggt cggaaaaaac ttatggaaac	180
ggcgacagcc ttaatacggg caaattgaag aacgacaagg tcagccgttt cgactttatc	240
cgtcaaateg aagtggacgg gcagctcatt accttggaga gcggagagtt ccaaataac	300
aaacaggacc actccgccgt cgttgcccta cagattgaaa aaatcaacaa ccccgacaaa	360
atcgacagcc tgataaacca acgctccttc cttgtcagcg gtttgggtgg agaacatacc	420
gccttcaacc aactgcccag cggcaaagcc gagtatcacg gcaaagcatt cagctccgac	480
gatgctggcg gaaaactgac ctataccata gatttcgccg ccaaacaggg acacggcaaa	540
atcgaacact tgaaaacacc cgagcaaaat gtcgagcttg cctccgccga actcaaagca	600
gatgaaaaat cacacgccgt cattttgggc gacacgcgct acggcgggcg agaaaaaggc	660
acttaccacc tcgccctttt cggcgaccgc gcccaagaaa tcgccggctc ggcaaccgtg	720
aagataaggg aaaagggttca cgaaatcggc atcgccggca aacagtag	768

<210> 106
 <211> 255
 <212> PRT
 <213> Neisseria meningitidis

<400> 106

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
 20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
 35 40 45

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
 85 90 95

Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile
 100 105 110

Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
 115 120 125

Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln
 130 135 140

Leu Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu
 180 185 190

Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile
 195 200 205

Leu Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu
 210 215 220

Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val
 225 230 235 240

Lys Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250 255

<210> 107

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 107

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atgagcagcg gagggcgcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc      120
aggaaaaacg agaaactgaa gctggcgggc caaggtgcgg aaaaaactta tggaaacggc      180
gacagcctta atacgggcaa attgaagaac gacaaggcca gccgtttcga ctttatccgt      240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa      300
caggaccact ccgccgtcgt tgccttacag attgaaaaaa tcaacaaccc cgacaaaatc      360
gacagcctga taaaccaacg ctcccttctt gtcagcgggt tgggtggaga acataccgcc      420
ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgat      480
gctggcgga aactgaccta taccatagat ttccgcgcca aacagggaca cggcaaaatc      540
gaacacttga aaacacccga gcaaaatgtc gagcttgctt ccgccgaact caaagcagat      600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact      660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag      720
ataagggaaa aggttcacga aatcggcata gccggcaaac agtag                          765

```

<210> 108

<211> 254

<212> PRT

<213> Neisseria meningitidis

<400> 108

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu

100

1	5	10	15
Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln	20	25	30
Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu	35	40	45
Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn	50	55	60
Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg	65	70	75
Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe	85	90	95
Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu	100	105	110
Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser	115	120	125
Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu	130	135	140
Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp	145	150	155
Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly	165	170	175
His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu	180	185	190
Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu	195	200	205
Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala	210	215	220
Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys	225	230	235
			240

101

Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 109

<211> 765

<212> DNA

<213> *Neisseria meningitidis*

<400> 109

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tgcagcagcg gagggcgcg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcgcgc      120
aggaaaaacg agaaactgaa gctggcgggc caaggtgcgg agaaaactta tggaaacggc      180
gacagcctca atacgggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt      240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa      300
caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc      360
gacagcctga taaaccaacg ctcccttctt gtcagcgggt tgggcggaga acataccgcc      420
ttcaaccaac tgccctgacg caaagccgag tatcacggca aagcattcag ctccgacgat      480
gctggcgga aactgaccta taccatagat ttcgccgcc aacagggaca cggcaaaatc      540
gaacacctga aaacacccga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat      600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcagcgaaga aaaaggcact      660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag      720
ataggggaaa aggttcacga aatcggcatc gccggcaaac agtag                          765

```

<210> 110

<211> 254

<212> PRT

<213> *Neisseria meningitidis*

<400> 110

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

102

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 111

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 111
 tgcggatcca gcggaggcgg cgggtgtcgcc gccgacatcg gcgcggggct tgccgatgca 60
 ctaaccgcac cgctcgacca taaagacaaa agtttgcagt ctttgacgct ggatcagtcc 120
 gtcaggaaaa acgagaaact gaagctggcg gcacaagggtg cggagaaaac ttatggaaac 180
 ggcgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgctt cgactttatc 240
 cgtcaaactc aagtggacgg gcagctcatt accttgagaga gcggagagtt ccaaataac 300
 aaacaggacc actccgccgt cgttgcccta cagattgaaa aaatcaacaa ccccgacaaa 360
 atcgacagcc tgataaacca acgctccttc cttgtcagcg gtttgggcgg agaacatacc 420
 gccttcaacc aactgcctga cggcaaagcc gagtatcacg gcaaagcatt cagctccgac 480
 gatgctggcg gaaaactgac ctataccata gatttcgccg ccaaacaggg acacggcaaa 540
 atcgaacacc tgaaaacacc cgagcaaaat gtcgagcttg ccgccgccga actcaaagca 600
 gatgaaaaat cacacgccgt cattttgggc gacacgcgct acggcagcga agaaaaaggc 660
 acttaccacc tcgccctttt cggcgaccgc gcccaagaaa tcgccggctc ggcaaccgtg 720
 aagatagggg aaaaggttca cgaaatcggc atcgccggca aacagtag 768

<210> 112
 <211> 255
 <212> PRT
 <213> *Neisseria meningitidis*

<400> 112
 Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15
 Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
 20 25 30
 Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
 35 40 45
 Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60
 Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80
 Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu

104

				85					90					95		
Phe	Gln	Ile	Tyr	Lys	Gln	Asp	His	Ser	Ala	Val	Val	Ala	Leu	Gln	Ile	
			100					105					110			
Glu	Lys	Ile	Asn	Asn	Pro	Asp	Lys	Ile	Asp	Ser	Leu	Ile	Asn	Gln	Arg	
		115					120					125				
Ser	Phe	Leu	Val	Ser	Gly	Leu	Gly	Gly	Glu	His	Thr	Ala	Phe	Asn	Gln	
	130					135					140					
Leu	Pro	Asp	Gly	Lys	Ala	Glu	Tyr	His	Gly	Lys	Ala	Phe	Ser	Ser	Asp	
145					150					155					160	
Asp	Ala	Gly	Gly	Lys	Leu	Thr	Tyr	Thr	Ile	Asp	Phe	Ala	Ala	Lys	Gln	
				165					170					175		
Gly	His	Gly	Lys	Ile	Glu	His	Leu	Lys	Thr	Pro	Glu	Gln	Asn	Val	Glu	
			180					185					190			
Leu	Ala	Ala	Ala	Glu	Leu	Lys	Ala	Asp	Glu	Lys	Ser	His	Ala	Val	Ile	
		195					200					205				
Leu	Gly	Asp	Thr	Arg	Tyr	Gly	Ser	Glu	Glu	Lys	Gly	Thr	Tyr	His	Leu	
	210					215					220					
Ala	Leu	Phe	Gly	Asp	Arg	Ala	Gln	Glu	Ile	Ala	Gly	Ser	Ala	Thr	Val	
225					230					235					240	
Lys	Ile	Gly	Glu	Lys	Val	His	Glu	Ile	Gly	Ile	Ala	Gly	Lys	Gln		
				245					250					255		

<210> 113

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 113

atgagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta 60

accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc 120

aqgaaaaacg agaaactgaa gctggcggca caaggtgcgg agaaaactta tggaaacggc 180

gacagcctca atacgggcaa attgaagaac gacaagggtca gccgcttcga ctttatccgt 240

105

```

caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa   300
caggaccact ccgcgcgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc   360
gacagcctga taaaccaacg ctcccttcctt gtcagcgggtt tgggcggaga acataccgcc   420
ttcaaccaac tgctgacggg caaagccgag tatcacggca aagcattcag ctccgacgat   480
gctggcgga aactgaccta taccatagat ttgcgcgcca aacagggaca cggcaaaatc   540
gaacacctga aaacacccga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat   600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcagcgaaga aaaaggcact   660
taccacctcg ccccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag   720
ataggggaaa aggttcacga aatcggcacg gccggcaaac agtag                       765

```

```

<210> 114
<211> 254
<212> PRT
<213> Neisseria meningitidis

<400> 114

```

```

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10           15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
          20           25           30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35           40           45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50           55           60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65           70           75           80

```

```

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
          85           90           95

```

```

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
          100          105          110

```

```

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
          115          120          125

```


106

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 115

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 115

tgcagcagcg gaggcggcgg tgctgccgcc gacatcggcg cggggccttgc cgatgcacta	60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc	120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc	180
gacagcctca atacgggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt	240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa	300
caggaccact ccgccgtcgt tgcctacag attgaaaaaa tcaacaaccc cgacaaaatc	360
gacagcctga taaaccaacg ctccttcctt gtcagcgggt tgggcggaga acataccgcc	420
ttcaaccaac tgctgacgg caaagccgag tatcacggca aagcattcag ctccgacgat	480
gctggcggaa aactgaccta taccatagat ttgccgccca aacagggaca cggcaaaatc	540

107

```

gaacacctga aaacacccga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat    600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcagcgaaga aaaaggcact    660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag    720
ataggggaaa aggttcacga aatcggcatc gccggcaaac agtag                      765

```

```

<210> 116
<211> 254
<212> PRT
<213> Neisseria meningitidis

```

```

<400> 116

```

```

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10           15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
          20           25           30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35           40           45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50           55           60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65           70           75           80

```

```

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
          85           90           95

```

```

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
          100          105          110

```

```

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
          115          120          125

```

```

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
          130          135          140

```

```

Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
145          150          155          160

```

```

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly

```


108

	165		170		175
His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu					
	180		185		190
Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu					
	195		200		205
Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala					
	210		215		220
Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys					
	225		230		235
					240
Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln					
	245		250		

<210> 117

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 117

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tgcggatcca gcggaggcgg cgggtgtcgcc gccgacatcg gcgcggggct tgccgatgca      60
ctaaccgcac cgctcgacca taaagacaaa agtttgcagt ctttgacgct ggatcagttcc      120
gtcaggaaaa acgagaaact gaagctggcg gcacaaggtg cggaaaaaac ttatggaaac      180
ggcgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgctt cgactttatc      240
cgtcaaatcg aagtggacgg gcagctcatt accttggaga gcggagagtt ccaaataac      300
aaacaggacc actcgcctgt cgttgcccta cagattgaaa aaatcaacaa ccccgacaaa      360
atcgacagcc tgataaacca acgctccttc cttgtcagcg gtttggggcg agaacatacc      420
gccttcaacc aactgctga cggcaaagcc gagtatcacg gcaaagcatt cagctccgac      480
gatgctggcg gaaaactgac ctataccata gatttcgccg ccaaacaggg acacggcaaa      540
atcgaacacc tgaaaacacc cgagcaaaat gtcgagcttg ccgccgccga actcaaagca      600
gatgaaaaat cacacgccgt cttttgggc gacacgcgt acggcagcga agaaaaaggc      660
acttaccacc tcgccctttt cggcgaccgc gcccaagaaa tcgccggctc ggcaaccgtg      720
aagatagggg aaaagggtca cgaaatcggc atcgccggca aacagtag      768

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<210> 118

109

<211> 255

<212> PRT

<213> Neisseria meningitidis

<400> 118

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
 20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
 35 40 45

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
 85 90 95

Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile
 100 105 110

Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
 115 120 125

Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln
 130 135 140

Leu Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu
 180 185 190

Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile
 195 200 205

110

Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu
 210 215 220

Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val
 225 230 235 240

Lys Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250 255

<210> 119

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 119

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atgagcagcg gaggcgcgcg tgtcgccgcc gacatcggcg cggggccttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcgcgc      120
aggaaaaacg agaaactgaa gctggcgggc caaggtgcgg aaaaaactta tggaaacggc      180
gacagcctca atacggggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt      240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa      300
caggaccact ccgccgtcgt tgccttacag attgaaaaaa tcaacaaccc cgacaaaatc      360
gacagcctga taaaccaacg ctcttctctt gtcagcgggt tgggcggaga acataccgcc      420
ttcaaccaac tgcctgacgg caaagccgag tatcacggca aagcattcag ctccgacgat      480
gctggcgga aactgaccta taccatagat ttcgccgcca aacagggaca cggcaaaatc      540
gaacacctga aaacacccga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat      600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcagcgaaga aaaaggcact      660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag      720
ataggggaaa aggttcacga aatcggcatc gccggcaaac agtag                          765

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<210> 120

<211> 254

<212> PRT

<213> Neisseria meningitidis

<400> 120

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

111

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln

112

245

250

<210> 121
 <211> 765
 <212> DNA
 <213> *Neisseria meningitidis*

<400> 121
 tgcagcagcg gaggcggcgg tgtcgccgcc gacatcgggc cggggccttgc cgatgcacta 60
 accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc 120
 aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc 180
 gacagcctca atacgggcaa attgaagaac gacaaggcca gccgcttcga ctttatccgt 240
 caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa 300
 caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc 360
 gacagcctga taaaccaacg ctcttctctt gtcagcgggt tgggcggaga acataccgcc 420
 ttcaaccaac tgctgacgg caaagccgag tatcacggca aagcattcag ctccgacgat 480
 gctggcggaa aactgacctt taccatagat ttccgcccca aacagggaca cggcaaaatc 540
 gaacacctga aaacacccga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat 600
 gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcagcgaaga aaaaggcact 660
 taccacctcg cctttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag 720
 ataggggaaa aggttcacga aatcggcatc gccggcaaac agtag 765

<210> 122
 <211> 254
 <212> PRT
 <213> *Neisseria meningitidis*

<400> 122

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

113

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
130 135 140

Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
180 185 190

Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
195 200 205

Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
225 230 235 240

Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
245 250

<210> 123

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 123

tgccgatcca gcggaggcgg cgggtgtcgcc gccgacatcg gcgcggggct tgccgatgca 60

114

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ctaaccgcac cgctcgacca taaagacaaa agtttgcagt ctttgacgct ggatcagtcc 120
gtcaggaaaa acgagaaact gaagctggcg gcacaaggtg cggaaaaaac ttatggaaac 180
ggcgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgctt cgactttatc 240
cgtcaaatcg aagtggacgg gcagctcatt accttggaga gcggagagtt ccaaataatac 300
aaacaggacc actccgccgt cgttgcccta cagattgaaa aaatcaacaa ccccgacaaa 360
atcgacagcc tgataaacca acgctccttc cttgtcagcg gtttgggagg agaacatacc 420
gccttcaacc aactgcctga cggcaaagcc gagtatcacg gcaaagcatt cagctccgac 480
gatgctggcg gaaaactgac ctataccata gatttcgccg ccaaacaggg acacggcaaa 540
atcgaacacc tgaaaacacc cgagcaaaat gtcgagcttg ccgccgccga actcaaagca 600
gatgaaaaat cacacgccgt cattttgggc gacacgcgct acggcagcga agaaaaaggc 660
acttaccacc tcgccctttt cggcgaccgc gcccaagaaa tcgccggctc ggcaaccgtg 720
aagatagggg aaaagggttca cgaaatcggc atcgccggca aacagtag 768

```

```

<210> 124
<211> 255
<212> PRT
<213> Neisseria meningitidis

<400> 124

```

```

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
1           5           10          15

```

```

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
          20           25           30

```

```

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
          35           40           45

```

```

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
          50           55           60

```

```

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
65           70           75           80

```

```

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
          85           90           95

```


115

Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile
 100 105 110

Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
 115 120 125

Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln
 130 135 140

Leu Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu
 180 185 190

Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile
 195 200 205

Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu
 210 215 220

Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val
 225 230 235 240

Lys Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250 255

<210> 125

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 125

atgagcagcg gaggcggcgg tgctgcgcgcc gacatcggcg cggggccttgc cgatgcacta 60

accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcgcgc 120

aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc 180

gacagcctca atacgggcaa attgaagaac gacaaggcca gccgcttcga ctttatccgt 240

caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa 300

caggaccact ccgccgtcgt tgcctacag attgaaaaaa tcaacaaccc cgacaaaatc 360

116

```

gacagcctga taaaccaacg ctccttcctt gtcagcgggtt tgggcggaga acataccgcc      420
ttcaaccaac tgctgacgg caaagccgag tatcacggca aagcattcag ctccgacgat      480
gctggcgga aactgacctt taccatagat ttccgcgcca aacagggaca cggcaaaatc      540
gaacacctga aaacacccga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat      600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcagcgaaga aaaaggcact      660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag      720
ataggggaaa aggttcacga aatcggcatc gccggcaaac agtag                          765

```

<210> 126

<211> 254

<212> PRT

<213> *Neisseria meningitidis*

<400> 126

```

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10           15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
          20           25           30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35           40           45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50           55           60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65           70           75           80

```

```

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
          85           90           95

```

```

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
          100          105          110

```

```

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
          115          120          125

```

```

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
          130          135          140

```


117

Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 127

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 127

tgcagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta	60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcgcgc	120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc	180
gacagcctca atacgggcaa attgaagaac gacaaggcca gccgcttcga ctttatccgt	240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa	300
caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc	360
gacagcctga taaaccaacg ctcttctctt gtcagcgggt tgggcggaga acataccgcc	420
ttcaaccaac tgctgacgg caaagccgag tatcacggca aagcattcag ctccgacgat	480
gctggcggaa aactgaccta taccatagat ttcgccgcc aacagggaca cggcaaaatc	540
gaacacctga aaacacccga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat	600
gaaaaatcac acgccgtcat tttgggcggac acgcgctacg gcagcgaaga aaaaggcact	660

118

taccacctcg ccccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag 720

ataggggaaa aggttcacga aatcggcatc gccggcaaac agtag 765

<210> 128

<211> 254

<212> PRT

<213> Neisseria meningitidis

<400> 128

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
130 135 140

Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
165 170 175

119

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 129

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 129

tgccgatcca gcggaggcgg cgggtgtcgcc gccgacatcg gcgcgggggct tgccgatgca	60
ctaaccgcac cgctcgacca taaagacaaa agtttgcagt ctttgacgct ggatcagtc	120
gtcaggaaaa acgagaaact gaagctggcg gcacaagggt cggaaaaaac ttatggaaac	180
ggcgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgctt cgactttatc	240
cgtcaaactc aagtggacgg gcagctcatt accttggaga gcggagagtt ccaaataac	300
aaacaggacc actccgccgt cgttgcccta cagattgaaa aaatcaacaa ccccgacaaa	360
atcgacagcc tgataaacca acgctccttc cttgtcagcg gtttggggcg agaacatacc	420
gccttcaacc aactgctga cggcaaagcc gagtatcac gcaaagcatt cagctccgac	480
gatgctggcg gaaaactgac ctataccata gatttcgccg ccaaacaggg acacggcaaa	540
atcgaacacc tgaaaacacc cgagcaaaat gtcgagcttg ccgccgccga actcaaagca	600
gatgaaaaat cacacgccgt cattttgggc gacacgcgt acggcagcga agaaaaaggc	660
acttaccacc tcgccctttt cggcgaccgc gcccaagaaa tcgccggctc ggcaaccgtg	720
aagatagggg aaaaggttca cgaaatcggc atcgccggca aacagtag	768

<210> 130

<211> 255

<212> PRT

<213> Neisseria meningitidis

120

<400> 130

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
 20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
 35 40 45

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
 85 90 95

Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile
 100 105 110

Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
 115 120 125

Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln
 130 135 140

Leu Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu
 180 185 190

Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile
 195 200 205

Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu
 210 215 220

121

Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val
 225 230 235 240

Lys Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250 255

<210> 131

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 131

atgagcagcg gaggcggcgg tgcgcgcgcc gacatcggcg cggggccttgc cgatgcacta 60
 accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc 120
 aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc 180
 gacagcctca atacgggcaa attgaagaac gacaaggcca gccgcttcga ctttatccgt 240
 caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa 300
 caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc 360
 gacagcctga taaaccaacg ctcttctctt gtcagcgggt tgggcggaga acataccgcc 420
 ttcaaccaac tgctgacgg caaagccgag tatcacggca aagcattcag ctccgacgat 480
 gctggcggaa aactgaccta taccatagat ttgcgcgcca aacagggaca cggcaaaatc 540
 gaacacctga aaacacccga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat 600
 gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcagcgaaga aaaaggcact 660
 taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag 720
 ataggggaaa aggttcacga aatcggcatc gccggcaaac agtag 765

<210> 132

<211> 254

<212> PRT

<213> Neisseria meningitidis

<400> 132

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

123

<210> 133
 <211> 765
 <212> DNA
 <213> *Neisseria meningitidis*

<400> 133
 tgcagcagcg gagggggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta 60
 accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc 120
 aggaaaaacg agaaactgaa gctggcgcca caaggtgcgg aaaaaactta tggaaacggc 180
 gacagcctca atacgggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt 240
 caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa 300
 caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc 360
 gacagcctga taaaccaacg ctcttctcctt gtcagcgggtt tgggcggaga acataccgcc 420
 ttcaaccaac tgcttgacgg caaagccgag tatcacggca aagcattcag ctccgacgat 480
 gctggcggaa aactgaccta taccatagat ttcgccgcc aacagggaca cggcaaaatc 540
 gaacacctga aaacacccga gcaaatgtc gagcttgccg ccgccgaact caaagcagat 600
 gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcagcgaaga aaaaggcact 660
 taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag 720
 ataggggaaa aggttcacga aatcggcatc gccggcaaac agtaa 765

<210> 134
 <211> 254
 <212> PRT
 <213> *Neisseria meningitidis*

<400> 134

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg

124

65 70 75 80
 Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95
 Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110
 Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125
 Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140
 Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160
 Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175
 His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190
 Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205
 Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220
 Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240
 Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 135

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 135

tgcggatcca gcggagggcg cggtgtcgcc gccgacatcg gcgcggggct tgccgatgca 60

ctaaccgcac cgctcgacca taaagacaaa agtttgagct ctttgacgct ggatcagtc 120

125

```

gtcaggaaaa acgagaaact gaagctggcg gcacaaggtg cggaaaaaac ttatggaaac   180
ggcgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgctt cgactttatc   240
cgtcaaatacg aagtggacgg gcagctcatt accttggaga gcggagagtt ccaaatatac   300
aaacaggacc actccgccgt cgttgcccta cagattgaaa aaatcaacaa ccccgacaaa   360
atcgacagcc tgataaacca acgctccttc cttgtcagcg gtttgggagg agaacatacc   420
gccttcaacc aactgcctga cggcaaagcc gagtatcacg gcaaagcatt cagctccgac   480
gatgctggcg gaaaactgac ctataccata gatttcgccg ccaaacaggg acacggcaaa   540
atcgaacacc tgaaaacacc cgagcaaaat gtcgagcttg ccgccgccga actcaaagca   600
gatgaaaaat cacacgccgt cattttgggc gacacgcgct acggcagcga agaaaaaggc   660
acttaccacc tcgccctttt cggcgaccgc gcccaagaaa tcgccggctc ggcaaccgtg   720
aagatagggg aaaaggttca cgaaatcggc atcgccggca aacagtaa               768

```

```

<210> 136
<211> 255
<212> PRT
<213> Neisseria meningitidis

```

```

<400> 136

```

```

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
1           5           10          15

```

```

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
          20          25          30

```

```

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
          35          40          45

```

```

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
          50          55          60

```

```

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
65           70           75          80

```

```

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
          85          90          95

```

```

Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile
          100         105         110

```


126

Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
 115 120 125

Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln
 130 135 140

Leu Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu
 180 185 190

Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile
 195 200 205

Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu
 210 215 220

Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val
 225 230 235 240

Lys Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250 255

<210> 137

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 137

atgagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta 60

accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcgcgc 120

aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc 180

gacagcctca atacgggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt 240

caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa 300

caggaccact ccgccgtcgt tgccttacag attgaaaaaa tcaacaaccc cgacaaaatc 360

gacagcctga taaaccaacg ctccttcctt gtcagcgggt tgggcggaga acataccgcc 420

127

```

ttcaaccaac tgctgacgg caaagccgag tatcacggca aagcattcag ctccgacgat      480
gctggcggaa aactgaccta taccatagat ttgcgcgcca aacagggaca cggcaaaatc      540
gaacacctga aaacacccga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat      600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcagcgaaga aaaaggcact      660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag      720
ataggggaaa aggttcacga aatcggcacg gccggcaaac agtaa                        765

```

```

<210> 138
<211> 254
<212> PRT
<213> Neisseria meningitidis

```

```

<400> 138

```

```

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1          5          10          15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
          20          25          30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35          40          45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50          55          60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65          70          75          80

```

```

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
          85          90          95

```

```

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
          100          105          110

```

```

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
          115          120          125

```

```

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
          130          135          140

```

```

Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp

```


128

145 150 155 160
 Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175
 His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190
 Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205
 Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220
 Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240
 Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 139

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 139

tgcagcagcg gagggcgcg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta 60
 accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc 120
 aggaaaaacg agaaactgaa gctggcgga caaggtgcgg aaaaaactta tggaaacggc 180
 gacagcctta atacgggcaa attgaagaac gacaaggtca gccgtttcga ctttatccgt 240
 caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa 300
 caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc 360
 gacagcctga taaaccaacg ctcttctctt gtcagcgggt tgggtggaga acataccgcc 420
 ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgat 480
 gctggcgga aactgaccta taccatagat ttcgccacca aacagggaca cggcaaaatc 540
 gaacacttga aaacacccga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat 600
 gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcagcgaaga aaaaggcact 660
 taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag 720

129

ataggggaaa aggttcacga aatcggcacg gccggcaaac agtag

765

<210> 140

<211> 254

<212> PRT

<213> Neisseria meningitidis

<400> 140

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Thr Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

130

Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 141
 <211> 768
 <212> DNA
 <213> *Neisseria meningitidis*

<400> 141
 tgcggatcca gcggaggcgg cgggtgtcgcc gccgacatcg gcgcgggggct tgccgatgca 60
 ctaaccgcac cgctcgacca taaagacaaa agtttgcagt ctttgacgct ggatcagtcc 120
 gtcaggaaaa acgagaaaact gaagctggcg gcacaagggtg cggaaaaaac ttatggaaac 180
 ggcgacagcc ttaatacggg caaattgaag aacgacaagg tcagccgttt cgactttatc 240
 cgtcaaatacg aagtggacgg gcagctcatt accttggaga gcggagagtt ccaaataac 300
 aaacaggacc actccgccgt cgttgcccta cagattgaaa aaatcaacaa ccccgacaaa 360
 atcgacagcc tgataaacca acgctccttc cttgtcagcg gtttgggtgg agaacatacc 420
 gccttcaacc aactgcccag cggcaaagcc gagtatcacg gcaaagcatt cagctccgac 480
 gatgctggcg gaaaactgac ctataccata gatttcgcca ccaaacaggg acacggcaaa 540
 atcgaacact tgaaaacacc cgagcaaaat gtcgagcttg ccgccgccga actcaaagca 600
 gatgaaaaat cacacgccgt cattttgggc gacacgcgct acggcagcga agaaaaaggc 660
 acttaccacc tcgccctttt cggcgaccgc gcccaagaaa tcgccggctc ggcaaccgtg 720
 aagatagggg aaaaggttca cgaaatcggc atcgccggca aacagtag 768

<210> 142
 <211> 255
 <212> PRT
 <213> *Neisseria meningitidis*

<400> 142

131

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15
 Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
 20 25 30
 Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
 35 40 45
 Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60
 Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80
 Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
 85 90 95
 Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile
 100 105 110
 Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
 115 120 125
 Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln
 130 135 140
 Leu Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp
 145 150 155 160
 Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Thr Lys Gln
 165 170 175
 Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu
 180 185 190
 Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile
 195 200 205
 Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu
 210 215 220
 Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val

132

225

230

235

240

Lys Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250 255

<210> 143

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 143

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atgagcagcg gagggcgcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc      120
aggaaaaacg agaaactgaa gctggcgggc caaggtgcgg aaaaaactta tggaaacggc      180
gacagcctta atacgggcaa attgaagaac gacaaggtca gccgtttcga ctttatccgt      240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa      300
caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc      360
gacagcctga taaaccaacg ctccctcctt gtcagcgggt tgggtggaga acataccgcc      420
ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgat      480
gctggcgga aactgaccta taccatagat ttccgccacca aacagggaca cggcaaaatc      540
gaacacttga aaacaccgga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat      600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcagcgaaga aaaaggcact      660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag      720
ataggggaaa aggttcacga aatcggcatc gccggcaaac agtag                          765

```

<210> 144

<211> 254

<212> PRT

<213> Neisseria meningitidis

<400> 144

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

133

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60
 Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80
 Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95
 Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110
 Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125
 Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140
 Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160
 Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Thr Lys Gln Gly
 165 170 175
 His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190
 Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205
 Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220
 Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240
 Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 145
 <211> 765
 <212> DNA

<213> *Neisseria meningitidis*

<400> 145

```

tgcagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggccttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc      120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc      180
gacagcctta atacgggcaa attgaagaac gacaaggcca gccgtttcga ctttatccgt      240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa      300
caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc      360
gacagcctga taaaccaacg ctccctcctt gtcagcgggt tgggtggaga acataccgcc      420
ttcaaccaac tgcccagcgg caaagccgag tatcaaggca aagcattcag ctccgacgat      480
gctggcggaa aactgaccta taccatagat ttcgccacca aacagggaca cggcaaaatc      540
gaacacttga aaacacccga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat      600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcagcgaaga aaaaggcact      660
taccacctcg cctttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag      720
ataggggaaa aggttcacga aatcggcatc gccggcaaac agtag                          765

```

<210> 146

<211> 254

<212> PRT

<213> *Neisseria meningitidis*

<400> 146

```

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10          15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
          20          25          30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35          40          45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50          55          60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65          70          75          80

```


135

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Thr Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 147

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 147

tgccgatcca gcggaggcgg cgggtgtcgcc gccgacatcg gcgcggggct tgccgatgca 60

ctaaccgcac cgctcgacca taaagacaaa agtttgcagt ctttgacgct ggatcagtcc 120

gtcaggaaaa acgagaaact gaagctggcg gcacaaggtg cggaaaaaac ttatggaaac 180

ggcgacagcc ttaatacggg caaattgaag aacgacaagg tcagccgttt cgactttatc 240

136

```

cgtcaaatacg aagtggacgg gcagctcatt accttggaga gcggagagtt ccaaataac 300
aaacaggacc actccgccgt cgttgcccta cagattgaaa aaatcaacaa ccccgacaaa 360
atcgacagcc tgataaacca acgctccttc cttgtcagcg gtttgggtgg agaacatacc 420
gccttcaacc aactgcccag cggcaaagcc gagtatcacg gcaaagcatt cagctccgac 480
gatgctggcg gaaaactgac ctataccata gatttcgcca ccaaacaggg acacggcaaa 540
atcgaacact tgaaaacacc cgagcaaaat gtcgagcttg ccgccgccga actcaaagca 600
gatgaaaaat cacacgccgt cattttgggc gacacgcgt acggcagcga agaaaaaggg 660
acttaccacc tcgccctttt cggcgaccgc gcccaagaaa tcgccggctc ggcaaccgtg 720
aagatagggg aaaagggtca cgaaatcggc atcgccggca aacagtag 768

```

<210> 148

<211> 255

<212> PRT

<213> Neisseria meningitidis

<400> 148

```

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
1           5           10           15

```

```

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
          20           25           30

```

```

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
          35           40           45

```

```

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
          50           55           60

```

```

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
          65           70           75           80

```

```

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
          85           90           95

```

```

Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile
          100          105          110

```

```

Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
          115          120          125

```


137

Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln
 130 135 140

Leu Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Thr Lys Gln
 165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu
 180 185 190

Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile
 195 200 205

Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu
 210 215 220

Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val
 225 230 235 240

Lys Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250 255

<210> 149

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 149

atgagcagcg gaggcggcgg tgctgcgccg gacatcggcg cggggcttgc cgatgcacta 60
 accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc 120
 aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc 180
 gacagcctta atacgggcaa attgaagaac gacaaggtca gccgtttcga ctttatccgt 240
 caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa 300
 caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc 360
 gacagcctga taaaccaacg ctccttcctt gtcagcgggt tgggtggaga acataccgcc 420
 ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgat 480
 gctggcggaa aactgaccta taccatagat ttcgccacca aacagggaca cggcaaaatc 540

138

gaacacttga aaacacccga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat 600
 gaaaaaatcac acgccgtcat tttggggcgac acgcgctacg gcagcgaaga aaaaggcact 660
 taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag 720
 ataggggaaa aggttcacga aatcggcatc gccggcaaac agtag 765

<210> 150

<211> 254

<212> PRT

<213> Neisseria meningitidis

<400> 150

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

139

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Thr Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 151

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 151

tgcagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta	60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc	120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc	180
gacagcctta atacgggcaa attgaagaac gacaaggtca gccgtttcga ctttatccgt	240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa	300
caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaacc cgcacaaatc	360
gacagcctga taaaccaacg ctcttctctt gtcagcgggt tgggtggaga acataccgcc	420
ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgat	480
gctggcggaa aactgaccta taccatagat ttcgccacca aacagggaca cggcaaaatc	540
gaacacttga aaacacccga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat	600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcagcgaaga aaaaggcact	660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag	720
ataggggaaa aggttcacga aatcggcatc gccggcaaac agtag	765

140

<210> 152
 <211> 254
 <212> PRT
 <213> Neisseria meningitidis

<400> 152

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Thr Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

141

Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 153

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 153

tgccgatcca gcggaggcgg cgggtgtcgcc gccgacatcg gcgcgggggt tgccgatgca	60
ctaaccgcac cgctcgacca taaagacaaa agtttgcagt ctttgacgct ggatcagtcc	120
gtcaggaaaa acgagaaaact gaagctggcg gcacaagggt cggaaaaaac ttatggaaac	180
ggcgacagcc ttaatacggg caaattgaag aacgacaagg tcagccggtt cgactttatc	240
cgtcaaactc aagtggacgg gcagctcatt accttggaga gcggagagtt ccaaataac	300
aaacaggacc actccgccgt cgttgcccta cagattgaaa aaatcaacaa ccccgacaaa	360
atcgacagcc tgataaacca acgctccttc cttgtcagcg gtttgggtgg agaacatacc	420
gccttcaacc aactgcccg cggaagacc gagtatcacg gcaaagcatt cagctccgac	480
gatgctggcg gaaaactgac ctataccata gatttcgcca ccaaagagg acacggcaaa	540
atcgaacact tgaaaacacc cgagcaaaat gtcgagcttg ccgccgccga actcaaagca	600
gatgaaaaat cacacgccgt cattttgggc gacacgcgt acggcagcga agaaaaaggc	660
acttaccacc tcgccctttt cggcgaccgc gcccaagaaa tcgccgggtc ggcaaccgtg	720
aagatagggg aaaaggttca cgaaatcggc atcgccggca aacagtag	768

<210> 154

<211> 255

<212> PRT

<213> Neisseria meningitidis

<400> 154

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15

142

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
 20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
 35 40 45

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
 85 90 95

Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile
 100 105 110

Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
 115 120 125

Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln
 130 135 140

Leu Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Thr Lys Gln
 165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu
 180 185 190

Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile
 195 200 205

Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu
 210 215 220

Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val
 225 230 235 240

143

Lys Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250 255

<210> 155

<211> 765

<212> DNA

<213> *Neisseria meningitidis*

<400> 155

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atgagcagcg gagggggcgg tgtcgccgcc gacatcggcg cggggccttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcgcgc      120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc      180
gacagcctta atacgggcaa attgaagaac gacaaggtca gccgtttoga ctttatccgt      240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagtcca aatatacaaa      300
caggaccact ccgccgtcgt tgcctacag attgaaaaaa tcaacaaccc cgacaaaatc      360
gacagcctga taaaccaacg ctccctcctt gtcagcgggt tgggtggaga acataccgcc      420
ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgat      480
gctggcggaa aactgaccta taccatagat ttccgccacca aacagggaca cggcaaaatc      540
gaacacttga aaacacccga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat      600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcagcgaaga aaaaggcact      660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag      720
ataggggaaa aggttcacga aatcggcatc gccggcaaac agtag                          765

```

<210> 156

<211> 254

<212> PRT

<213> *Neisseria meningitidis*

<400> 156

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn

144

50

55

60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Thr Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 157

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 157

145

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tgcagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta      60
accgcaccgc tcgactataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc      120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc      180
gacagcctca atacgggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt      240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa      300
caggaccact ccgccgtcgt tgccctatag attgaaaaaa tcaacaaccc cgacaaaatc      360
gacagcctga taaaccaacg ctcccttctt gtcagcgggt tgggtggaga acataccgcc      420
ttcaaccaac tgcccgggcg caaagccgag tatcacggca aagcattcag ctccgacgat      480
gctggcggaa aactgaccta taccatagat ttcgccgcc aacagggaca cggcaaaatc      540
gaacacctga aaacaccgga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat      600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcagcgaaga aaaaggcact      660
taccacctcg cccttttcgg cgaccgcgct caagaaatcg ccggctcggc aaccgtgaag      720
ataggggaaa aggttcacga aatcggcatc gccggcaaac agtag                        765

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<210> 158

<211> 253

<212> PRT

<213> *Neisseria meningitidis*

<400> 158

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Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10           15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp Tyr Lys Asp Lys Ser Leu Gln
          20           25           30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35           40           45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50           55           60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65           70           75           80

```

```

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
          85           90           95

```


146

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Ile Glu Lys
 100 105 110

Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser Phe
 115 120 125

Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu Pro
 130 135 140

Gly Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp Ala
 145 150 155 160

Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly His
 165 170 175

Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu Ala
 180 185 190

Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu Gly
 195 200 205

Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala Leu
 210 215 220

Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys Ile
 225 230 235 240

Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 159

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 159

tgcgatcca gcggagggcg cggtgtcgcc gccgacatcg gcgcggggct tgccgatgca 60

ctaaccgcac cgctcgacta taaagacaaa agtttgagct ctttgacgct ggatcagtc 120

gtcaggaaaa acgagaaact gaagctggcg gcacaaggtg cggaaaaaac ttatggaaac 180

ggcgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgctt cgactttatc 240

cgtcaaatacg aagtggacgg gcagctcatt accttgagaga gcggagagtt ccaaataac 300

147

```

aacaggacc actccgccgt cgttgcccta tagattgaaa aaatcaacaa ccccgacaaa   360
atcgacagcc tgataaacca acgctccttc cttgtcagcg gtttggtgga agaacatacc   420
gccttcaacc aactgcccgg cggcaaagcc gagtatcacg gcaaagcatt cagctccgac   480
gatgctggcg gaaaactgac ctataccata gatttcgccg ccaaacaggg acacggcaaa   540
atcgaacacc tgaaaacacc cgagcaaaat gtcgagcttg ccgccgccga actcaaagca   600
gatgaaaaat cacacgccgt cattttgggc gacacgcgct acggcagcga agaaaaaggc   660
acttaccacc tcgccctttt cggcgaccgc gctcaagaaa tcgccggctc ggcaaccgtg   720
aagatagggg aaaaggttca cgaaatcggc atcgccggca aacagtag               768

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<210> 160

<211> 254

<212> PRT

<213> *Neisseria meningitidis*

<400> 160

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp Tyr Lys Asp Lys Ser Leu
 20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
 35 40 45

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
 85 90 95

Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu

148

130 135 140
 Pro Gly Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160
 Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175
 His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190
 Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205
 Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220
 Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240
 Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 161

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 161

atgagcagcg gaggcggcgg tgctcgccgcc gacatcgggc cggggcttgc cgatgcacta 60
 accgcaccgc tcgactataa agacaaaagt ttgcagtctt tgacgctgga tcagtcgcgc 120
 aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc 180
 gacagcctca atacgggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt 240
 caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa 300
 caggaccact ccgccgtcgt tgccttatag attgaaaaaa tcaacaacc cgacaaaatc 360
 gacagcctga taaaccaacg ctccctcctt gtcagcgggt tgggtggaga acataccgcc 420
 ttcaaccaac tgcccggcgg caaagccgag tatcacggca aagcattcag ctccgacgat 480
 gctggcggaa aactgaccta taccatagat ttcgccgcca aacagggaca cggcaaaatc 540
 gaacacctga aaacacccga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat 600

149

gaaaaatcac acgcgcgtcat ttgggcgac acgcgctacg gcagcgaaga aaaaggcact 660
 taccacctcg cccttttcgg cgaccgcgt caagaaatcg ccggctcggc aaccgtgaag 720
 ataggggaaa aggttcacga aatcggcac gccggcaaac agtag 765

<210> 162
 <211> 253
 <212> PRT
 <213> Neisseria meningitidis

<400> 162

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp Tyr Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Ile Glu Lys
 100 105 110

Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser Phe
 115 120 125

Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu Pro
 130 135 140

Gly Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp Ala
 145 150 155 160

Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly His
 165 170 175

150

Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu Ala
 180 185 190

Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu Gly
 195 200 205

Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala Leu
 210 215 220

Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys Ile
 225 230 235 240

Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 163

<211> 765

<212> DNA

<213> *Neisseria meningitidis*

<400> 163

tgcagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta 60
 accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc 120
 aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc 180
 gacagcctca atacgggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt 240
 caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa 300
 caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaacct cgacaaaatc 360
 gacagcctga taaaccgacg ctcccttctt gtcagcgggt tgggcggaga acataccgcc 420
 ttcaaccaac tgcttgacgg caaagccgag tatcacggca aagcattcag ctccgacgat 480
 gctggcggaa aactgaccta taccatagat ttcgccgcca aacagggaca cggcaaaatc 540
 gaacacctga aaacacccga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat 600
 gaaaaatcac acgccgtcat ttggggcgac acgcgctacg gcagcgaaga aaaaggcact 660
 taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag 720
 ataggggaaa aggttcacga aatcggcatc gccggcaaac agtag 765

<210> 164

<211> 254

<212> PRT

151

<213> Neisseria meningitidis

<400> 164

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Arg Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala

152

210 215 220
 Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 165
 <211> 768
 <212> DNA
 <213> Neisseria meningitidis

<400> 165
 tgcggatcca gcggaggcgg cgggtgtcgcc gccgacatcg gcgcgggggct tgccgatgca 60
 ctaaccgcac cgctcgacca taaagacaaa agtttgcagt ctttgacgct ggatcagtc 120
 gtcaggaaaa acgagaaact gaagctggcg gcacaagggtg cggaaaaaac ttatggaaac 180
 ggcgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgctt cgactttatc 240
 cgtcaaactg aagtggacgg gcagctcatt accttggaga gcggagagtt ccaaataac 300
 aaacaggacc actccgccgt cgttgcccta cagattgaaa aaatcaacaa ccccgacaaa 360
 atcgacagcc tgataaacgg acgctccttc cttgtcagcg gtttggggcg agaacatacc 420
 gccttcaacc aactgcctga cggcaaagcc gagtatcacg gcaaagcatt cagctccgac 480
 gatgctggcg gaaaactgac ctataccata gatttcgccg ccaaacaggg acacggcaaa 540
 atcgaacacc tgaaaacacc cgagcaaaat gtcgagcttg ccgccgccga actcaaagca 600
 gatgaaaaat cacacgccgt cattttgggc gacacgcgt acggcagcga agaaaaaggc 660
 acttaccacc tcgccctttt cggcgaccgc gcccaagaaa tcgccggctc ggcaaccgtg 720
 aagatagggg aaaaggttca cgaaatcggc atcgccggca aacagtag 768

<210> 166
 <211> 255
 <212> PRT
 <213> Neisseria meningitidis

<400> 166

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
 20 25 30

154

<210> 167
 <211> 765
 <212> DNA
 <213> *Neisseria meningitidis*

<400> 167
 atgagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta 60
 accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcgcgc 120
 aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc 180
 gacagcctca atacgggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt 240
 caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa 300
 caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc 360
 gacagcctga taaaccgacg ctccctcctt gtcagcgggt tgggcggaga acataccgcc 420
 ttcaaccaac tgcctgacgg caaagccgag tatcacggca aagcattcag ctccgacgat 480
 gctggcggaa aactgaccta taccatagat ttccgcccca aacagggaca cggcaaaaatc 540
 gaacacctga aaacacccga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat 600
 gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcagcgaaga aaaaggcact 660
 taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag 720
 ataggggaaa aggttcacga aatcggcatc gccggcaaac agtag 765

<210> 168
 <211> 254
 <212> PRT
 <213> *Neisseria meningitidis*

<400> 168
 Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15
 Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30
 Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45
 Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

155

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Arg Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240

Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 169

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 169

tgcagcagcg gaggcggcgg tgctgccgcc gacatcggcg cggggcttgc cgatgcacta 60

accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc 120

156

```

aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc   180
gacagcctca atacgggcaa attgaagaac gacaagggtca gccgcttcga ctttatccgt   240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaaa   300
caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc   360
gacagcctga taaaccaacg ctcttctcctt gtcagcgggtt tgggcggaga acataccgcc   420
ttcaaccaac tgctgacgg caaagccgag tatcacggca aagcattcag ctccgacgat   480
gctggcggaa aactgaccta taccatagat ttgcgcgcca aacagggaca cggcaaaatc   540
gaacacctga aaacacccga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat   600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcagcgaaga aaaaggcact   660
taccacctcg cctttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtggag   720
ataggggaaa aggttcacga aatcggcatc gccggcaaac agtag                       765

```

<210> 170

<211> 254

<212> PRT

<213> *Neisseria meningitidis*

<400> 170

```

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10           15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
          20           25           30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35           40           45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50           55           60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65           70           75           80

```

```

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
          85           90           95

```

```

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
          100          105          110

```


157

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Glu
 225 230 235 240

Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 171

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 171

tgcggatcca gcgaggcg cggtgtcgcc gccgacatcg gcgcggggct tgccgatgca	60
ctaaccgcac cgctcgacca taaagacaaa agtttgcagt ctttgacgct ggatcagtcc	120
gtcaggaaaa acgagaaact gaagctggcg gcacaagggt cggaaaaaac ttatggaaac	180
ggcgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgctt cgactttatc	240
cgtcaaatcg aagtggacgg gcagctcatt accttggaga gcggagagtt ccaaataac	300
aaacaggacc actccgccgt cgttgcccta cagattgaaa aaatcaacaa ccccgacaaa	360
atcgacagcc tgataaacca acgtccttc cttgtcagcg gtttgggcgg agaacatacc	420

158

```

gccttcaacc aactgctga cggcaaagcc gagtatcacg gcaaagcatt cagctccgac      480
gatgctggcg gaaaactgac ctataccata gatttcgccg ccaaacaggg acacggcaaa      540
atcgaacacc tgaaaacacc cgagcaaaat gtcgagcttg ccgccgccga actcaaagca      600
gatgaaaaat cacacgccgt cattttgggc gacacgcgct acggcagcga agaaaaaggc      660
acttaccacc tcgccctttt cggcgaccgc gcccaagaaa tcgccggctc ggcaaccgtg      720
gagatagggg aaaagggttca cgaaatcggc atcgccggca aacagtag                    768

```

```

<210> 172
<211> 255
<212> PRT
<213> Neisseria meningitidis

```

```

<400> 172

```

```

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
1           5           10           15

```

```

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
          20           25           30

```

```

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
          35           40           45

```

```

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
          50           55           60

```

```

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
65           70           75           80

```

```

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
          85           90           95

```

```

Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile
          100          105          110

```

```

Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
          115          120          125

```

```

Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln
          130          135          140

```


159

Leu Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu
 180 185 190

Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile
 195 200 205

Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu
 210 215 220

Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val
 225 230 235 240

Glu Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250 255

<210> 173

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 173

atgagcagcg gaggcggcgg tgctcgccgcc gacatcggcg cggggcttgc cgatgcacta	60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc	120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc	180
gacagcctca atacgggcaa attgaagaac gacaagggtca gccgcttcga ctttatccgt	240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa	300
caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc	360
gacagcctga taaaccaacg ctcccttccct gtcagcgggt tgggcggaga acataccgcc	420
ttcaaccaac tgctgacgg caaagccgag tatcacggca aagcattcag ctccgacgat	480
gctggcggaa aactgaccta taccatagat ttcgccgcc aacagggaca cggcaaaatc	540
gaacacctga aaacacccga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat	600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcagcgaaga aaaaggcact	660
taccacctcg cctttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtggag	720

160

ataggggaaa aggttcacga aatcggcacg gccggcaaac agtag

765

<210> 174

<211> 254

<212> PRT

<213> Neisseria meningitidis

<400> 174

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140

Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190

161

Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Glu
 225 230 235 240

Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 175

<211> 768

<212> DNA

<213> *Neisseria meningitidis*

<400> 175

tgcagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cgggtgcttgc cgatgcacta	60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc	120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc	180
gacagcctca atacgggcaa attgaagaac gacaagggtca gccgcttcga ctttatccgt	240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca agtgtacaaa	300
caaagccatt ccgccttaac cgcccttcag accgagcaag tacaagattc ggagcattca	360
gggaagatgg ttgcgaaacg ccagttcaga atcggcgata tagcgggtga acatacatct	420
tttgacaagc ttcccgaagg cggcagggcg acatatcgcg ggacggcatt cggttcagac	480
gatgccagtg gaaaactgac ctacaccata gatttcgccg ccaagcaggg acacggcaaa	540
atcgaacatt tgaaatcgcc agaactcaat gttgacctgg ccgcctccga tatcaagccg	600
gataaaaaac gccatgccgt catcagcggg tccgtccttt acaaccaagc cgagaaaggc	660
agttactctc taggcatctt tggcgggcaa gcccaggaag ttgccggcag cgcagaagtg	720
gaaaccgcaa acggcatacg ccatatcggg cttgccgccca agcagtaa	768

<210> 176

<211> 255

<212> PRT

<213> *Neisseria meningitidis*

<400> 176

162

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Val Leu
 1 5 10 15
 Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30
 Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45
 Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60
 Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80
 Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95
 Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu
 100 105 110
 Gln Val Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln
 115 120 125
 Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
 130 135 140
 Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160
 Asp Ala Ser Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175
 Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp
 180 185 190
 Leu Ala Ala Ser Asp Ile Lys Pro Asp Lys Lys Arg His Ala Val Ile
 195 200 205
 Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu
 210 215 220

163

Gly Ile Phe Gly Gly Gln Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240

Glu Thr Ala Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 177
 <211> 771
 <212> DNA
 <213> Neisseria meningitidis

<400> 177
 tgcggatcca gcggaggcgg cgggtgtcgcc gccgacatcg gcgcggtgct tgccgatgca 60
 ctaaccgcac cgctcgacca taaagacaaa agtttgagct ctttgacgct ggatcagtc 120
 gtcaggaaaa acgagaaact gaagctggcg gcacaagggtg cggaaaaaac ttatggaaac 180
 ggcgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgctt cgactttatc 240
 cgtcaaactc aagtggacgg gcagctcatt accttgagga gcggagagtt ccaagtgtac 300
 aaacaaagcc attccgcctt aaccgccctt cagaccgagc aagtacaaga ttcggagcat 360
 tcagggaaga tggttgcgaa acgccagttc agaatcggcg atatagcggg tgaacataca 420
 tcttttgaca agcttcccgga aggcggcagg gcgacatatc gcgggacggc attcggttca 480
 gacgatgcca gtggaaaact gacctacacc atagatttcg ccgccaagca gggacacggc 540
 aaaatcgaac atttgaaatc gccagaactc aatgttgacc tggccgcctc cgatatcaag 600
 ccggataaaa aacgccatgc cgtcatcagc ggttccgtcc tttacaacca agccgagaaa 660
 ggcagttact ctctaggcat ctttggcggg caagcccagg aagttgccgg cagcgcagaa 720
 gtggaaaccg caaacggcat acgcatatc ggtcttgccg ccaagcagta a 771

<210> 178
 <211> 256
 <212> PRT
 <213> Neisseria meningitidis

<400> 178

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Val
 1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
 20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys

164

35 40 45
 Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60
 Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80
 Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
 85 90 95
 Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr
 100 105 110
 Glu Gln Val Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg
 115 120 125
 Gln Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys
 130 135 140
 Leu Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser
 145 150 155 160
 Asp Asp Ala Ser Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys
 165 170 175
 Gln Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val
 180 185 190
 Asp Leu Ala Ala Ser Asp Ile Lys Pro Asp Lys Lys Arg His Ala Val
 195 200 205
 Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser
 210 215 220
 Leu Gly Ile Phe Gly Gly Gln Ala Gln Glu Val Ala Gly Ser Ala Glu
 225 230 235 240
 Val Glu Thr Ala Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 179

<211> 768

165

<212> DNA

<213> *Neisseria meningitidis*

<400> 179

```

atgagcagcg gagggggcgg tgtcgccgcc gacatcggcg cggtgcttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc      120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc      180
gacagcctca atacgggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt      240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca agtgtacaaa      300
caaagccatt ccgccttaac cgcccttcag accgagcaag tacaagattc ggagcattca      360
gggaagatgg ttgcgaaacg ccagttcaga atcggcgata tagcgggtga acatacatct      420
tttgacaagc ttcccgaagg cggcagggcg acatatcgcg ggacggcatt cggttcagac      480
gatgccagtg gaaaactgac ctacaccata gatttcgccg ccaagcaggg acacggcaaa      540
atcgaacatt tgaaatcgcc agaactcaat gttgacctgg ccgcctccga tatcaagccg      600
gataaaaaac gccatgccgt catcagcggg tccgtccttt acaaccaagc cgagaaaggc      660
agttactctc taggcattct tggcgggcaa gccaggaag ttgccggcag cgcagaagtg      720
gaaaccgcaa acggcatacg ccatatcggt cttgccgcc aagcagtaa      768

```

<210> 180

<211> 255

<212> PRT

<213> *Neisseria meningitidis*

<400> 180

```

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Val Leu
1           5           10           15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
          20           25           30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35           40           45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50           55           60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65           70           75           80

```


166

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu
 100 105 110

Gln Val Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln
 115 120 125

Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
 130 135 140

Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160

Asp Ala Ser Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp
 180 185 190

Leu Ala Ala Ser Asp Ile Lys Pro Asp Lys Lys Arg His Ala Val Ile
 195 200 205

Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu
 210 215 220

Gly Ile Phe Gly Gly Gln Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240

Glu Thr Ala Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 181

<211> 747

<212> DNA

<213> Neisseria meningitidis

<400> 181

tgcagcagcg gagggggtgg tgtcgccgcc gacatcggtg cggggcttgc cgatgcacta 60

accgcaccgc tcgaccataa agacaaaggt ttgcagtctt tgacgctgga tcagtcctgc 120

aggaaaaacg agaaactgaa gctggcggca caagggtcggg aaaaaactta tggaaacggt 180

167

```

gacagcctca atacgggcaa attgaagaac gacaaggtca gccgtttcga ctttatccgc      240
caaatcgaag tggacgggca gctcattacc ttggagagtg gagagttcca agtatacaaaa      300
caaagccatt ccgccttaac cgcctttcag accgagcaaa tacaagattc ggagcattcc      360
gggaagatgg ttgcgaaacg ccagttcaga atcggcgaca tagcggggcg acatacatct      420
tttgacaagc ttcccgaagg cggcagggcg acatatcgcg ggacggcggt cggttcagac      480
gatgccggcg gaaaactgac ctacaccata gatttcgccg ccaagcaggg aaacggcaaa      540
atcgaacatt tgaaatcgcc agaactcaat gtcgacctgg ccgccgccga tatcaagccg      600
gatggaaaac gccatgccgt catcagcggg tccgtccttt acaaccaagc cgagaaaggc      660
agttactccc tcggtatctt tggcggaaaa gccaggaag ttgccggcag cgcggaagtg      720
aaaaccgtaa acggcatacg ccatatc                                     747

```

```

<210> 182
<211> 249
<212> PRT
<213> Neisseria meningitidis

```

```

<400> 182

```

```

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10           15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln
          20           25           30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35           40           45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50           55           60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65           70           75           80

```

```

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
          85           90           95

```

```

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln Thr Glu
          100          105          110

```

```

Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln

```


168

115 120 125
 Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
 130 135 140
 Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160
 Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175
 Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp
 180 185 190
 Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val Ile
 195 200 205
 Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu
 210 215 220
 Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240
 Lys Thr Val Asn Gly Ile Arg His Ile
 245

<210> 183

<211> 750

<212> DNA

<213> Neisseria meningitidis

<400> 183

tgcggatcca gcggaggggg tggtgtcgcc gccgacatcg gtgcggggct tgccgatgca 60
 ctaaccgcac cgctcgacca taaagacaaa ggtttgcagt ctttgacgct ggatcagttc 120
 gtcaggaaaa acgagaaact gaagctggcg gcacaagggt cggaaaaaac ttatggaaac 180
 ggtgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgttt cgactttatc 240
 cgccaaatcg aagtggacgg gcagctcatt accttgagga gtggagagtt ccaagtatac 300
 aaacaaagcc attccgcctt aaccgccttt cagaccgagc aaatacaaga ttcggagcat 360
 tccgggaaga tggttgcgaa acgccagttc agaatcgggc acatagcggg cgaacatata 420
 tcttttgaca agcttccccga aggcggcagg gcgacatatc gcgggacggc gttcggttca 480

169

gacgatgccg gcggaaaact gacctacacc atagatttcg ccgccaagca gggaaacggc 540
 aaaatcgaac atttgaaatc gccagaactc aatgtcgacc tggccgccgc cgatatcaag 600
 ccggatggaa aacgccatgc cgtcatcagc ggttccgtcc tttaacaacca agccgagaaa 660
 ggcagttact ccctcgggat ctttggcgga aaagcccagg aagttgccgg cagcgcggaa 720
 gtgaaaaccg taaacggcat acgcatatc 750

<210> 184
 <211> 250
 <212> PRT
 <213> Neisseria meningitidis

<400> 184

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15
 Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu
 20 25 30
 Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
 35 40 45
 Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60
 Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80
 Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
 85 90 95
 Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln Thr
 100 105 110
 Glu Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg
 115 120 125
 Gln Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys
 130 135 140
 Leu Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser
 145 150 155 160

170

Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys
 165 170 175

Gln Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val
 180 185 190

Asp Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val
 195 200 205

Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser
 210 215 220

Leu Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu
 225 230 235 240

Val Lys Thr Val Asn Gly Ile Arg His Ile
 245 250

<210> 185

<211> 747

<212> DNA

<213> Neisseria meningitidis

<400> 185

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atgagcagcg gagggggtgg tgtcgccgcc gacatcggtg cggggcttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaggt ttgcagtctt tgacgctgga tcagtccgtc      120
aggaaaaacg agaaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggt      180
gacagcctca atacgggcaa attgaagaac gacaagggtca gccgtttcga ctttatccgc      240
caaatcgaag tggacgggca gtcattacc ttggagagtg gagagttcca agtatacaaa      300
caaagccatt ccgccttaac cgcctttcag accgagcaaa tacaagattc ggagcattcc      360
gggaagatgg ttgcgaaacg ccagttcaga atcggcgaca tagcgggcca acatacatct      420
tttgacaagc ttcccgaagg cggcagggcg acatatcgcg ggacggcggt cggttcagac      480
gatgccggcg gaaaactgac ctacaccata gatttcgccg ccaagcaggg aaacggcaaa      540
atcgaacatt tgaaatcgcc agaactcaat gtcgacctgg ccgccgccga tatcaagccg      600
gatggaaaac gccatgccgt catcagcggg tccgtccttt acaaccaagc cgagaaaggc      660
agttactccc tcggtatctt tggcggaaaa gcccggaag ttgccggcag cgcggaagtg      720
aaaaccgtaa acggcatacg ccatatc                                     747

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171

<210> 186
 <211> 249
 <212> PRT
 <213> Neisseria meningitidis

<400> 186

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln Thr Glu
 100 105 110

Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln
 115 120 125

Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
 130 135 140

Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp
 180 185 190

Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val Ile

172

195 200 205
 Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu
 210 215 220
 Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240
 Lys Thr Val Asn Gly Ile Arg His Ile
 245

<210> 187
 <211> 747
 <212> DNA
 <213> *Neisseria meningitidis*
 <400> 187
 tgcagcagcg gagggggtgg tgtcgccgcc gacatcggtg cggggcttgc cgatgcacta 60
 accgcaccgc tcgaccataa agacaaaggt ttgcagtctt tgacgctgga tcagtcgcgc 120
 aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggt 180
 gacagcctca atacgggcaa attgaagaac gacaaggcca gccgtttcga ctttatccgc 240
 caaatcgaag tggacgggca gctcattacc ttggagagtg gagagttcca agtatacaaa 300
 caaagccatt ccgccttaac cgcctttcag accgagcaaa tacaagattc ggagcattcc 360
 gggaagatgg ttgcgaaacg ccagttcaga atcggcgaca tagcgggcca acatacatct 420
 tttgacaagc ttcccgaagg cggcagggcg acatatcgcg ggacggcggt cggttcagac 480
 gatgccggcg gaaaactgac ctacaccata gatttcgccg ccaagcaggg aaacggcaaa 540
 atcgaacatt tgaaatcgcc agaactcaat gtcgacctgg ccgccgccga tatcaagccg 600
 gatggaaaac gccatgccgt catcagcggg tccgtccttt acaaccaagc cgagaaaggc 660
 agttactccc tcggtatctt tggcggaaaa gccccaggaag ttgccggcag cgcggaagtg 720
 aaaaccgtaa acggcatacg ccatatc 747

<210> 188
 <211> 249
 <212> PRT
 <213> *Neisseria meningitidis*

<400> 188

Cys Ser Ser Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

173

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln Thr Glu
 100 105 110

Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln
 115 120 125

Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
 130 135 140

Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp
 180 185 190

Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val Ile
 195 200 205

Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu
 210 215 220

Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240

Lys Thr Val Asn Gly Ile Arg His Ile
245

<210> 189

<211> 750

<212> DNA

<213> *Neisseria meningitidis*

<400> 189

tgccgatcca	gcggaggggg	tggtgtcgcc	gccgacatcg	gtgcggggct	tgccgatgca	60
ctaaccgcac	cgctcgacca	taaagacaaa	ggtttgcagt	ctttgacgct	ggatcagtc	120
gtcaggaaaa	acgagaaaact	gaagctggcg	gcacaagggtg	cggaaaaaac	ttatggaaac	180
ggtgacagcc	tcaatacggg	caaattgaag	aacgacaagg	tcagccgttt	cgactttatc	240
cgccaaatcg	aagtggacgg	gcagctcatt	accttggaga	gtggagagtt	ccaagtatac	300
aaacaaagcc	attccgcctt	aaccgccttt	cagaccgagc	aaatacaaga	ttcggagcat	360
tccgggaaga	tggttgcgaa	acgccagttc	agaatcggcg	acatagcggg	cgaacataca	420
tcttttgaca	agcttcccg	aggcggcagg	gcgacatata	gcgggacggc	gttcggttca	480
gacgatgccg	gcggaaaact	gacctacacc	atagatttcg	ccgccaagca	gggaaacggc	540
aaaatcgaac	atttgaaatc	gccagaactc	aatgtcgacc	tgcccgccgc	cgatatcaag	600
ccggatggaa	aacgccatgc	cgtcatcagc	ggttccgtcc	tttacaacca	agccgagaaa	660
ggcagttact	ccctcggat	ctttggcgga	aaagcccagg	aagttgccgg	cagcgcgga	720
gtgaaaaccg	taaacggcat	acgccatata				750

<210> 190

<211> 250

<212> PRT

<213> *Neisseria meningitidis*

<400> 190

Cys	Gly	Ser	Ser	Gly	Gly	Gly	Gly	Val	Ala	Ala	Asp	Ile	Gly	Ala	Gly
1				5					10					15	

Leu	Ala	Asp	Ala	Leu	Thr	Ala	Pro	Leu	Asp	His	Lys	Asp	Lys	Gly	Leu
			20					25					30		

Gln	Ser	Leu	Thr	Leu	Asp	Gln	Ser	Val	Arg	Lys	Asn	Glu	Lys	Leu	Lys
		35						40				45			

175

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
 85 90 95

Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln Thr
 100 105 110

Glu Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg
 115 120 125

Gln Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys
 130 135 140

Leu Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser
 145 150 155 160

Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys
 165 170 175

Gln Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val
 180 185 190

Asp Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val
 195 200 205

Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser
 210 215 220

Leu Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu
 225 230 235 240

Val Lys Thr Val Asn Gly Ile Arg His Ile
 245 250

<210> 191

<211> 747

<212> DNA

<213> Neisseria meningitidis

176

<400> 191
 atgagcagcg gagggggtgg tgtcgccgcc gacatcggtg cggggcttgc cgatgcacta 60
 accgcaccgc tcgaccataa agacaaaggt ttgcagtctt tgacgctgga tcagtccgtc 120
 aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggt 180
 gacagcctca atacgggcaa attgaagaac gacaaggcca gccgtttcga ctttatccgc 240
 caaatcgaag tggacgggca gctcattacc ttggagagtg gagagttcca agtatacaaa 300
 caaagccatt ccgccttaac cgcttttcag accgagcaaa tacaagattc ggagcattcc 360
 gggaagatgg ttgcgaaacg ccagttcaga atcggcgaca tagcgggcca acatacatct 420
 ttgacaagc ttcccgaagg cggcagggcg acatatcgcg ggacggcggt cggttcagac 480
 gatgccggcg gaaaactgac ctacaccata gatttcgccg ccaagcaggg aaacggcaaa 540
 atcgaacatt tgaaatcgcc agaactcaat gtcgacctgg ccgccgccga tatcaagccg 600
 gatggaaaac gccatgccgt catcagcggg tccgtccttt acaaccaagc cgagaaaggc 660
 agttactccc tcggtatctt tggcggaaaa gccaggaag ttgccggcag cgcggaagtg 720
 aaaaccgtaa acggcatacg ccatatc 747

<210> 192
 <211> 249
 <212> PRT
 <213> Neisseria meningitidis

<400> 192
 Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15
 Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln
 20 25 30
 Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45
 Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60
 Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80
 Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

177

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln Thr Glu
 100 105 110

Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln
 115 120 125

Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
 130 135 140

Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp
 180 185 190

Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val Ile
 195 200 205

Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu
 210 215 220

Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240

Lys Thr Val Asn Gly Ile Arg His Ile
 245

<210> 193

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 193

tgcagcagcg gagggggtgg tgtcgccgcc gacatcggtg cggggcttgc cgatgcacta	60
accgcaccgc tcgaccataa agacaaaaggt ttgcagtctt tgacgctgga tcagtccgtc	120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggt	180
gacagcctca atacgggcaa attgaagaac gacaaggtca gccgtttcga ctttatccgc	240
caaatcgaag tggacgggca gctcattacc ttggagagtg gagagttcca agtatacaaa	300

178

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caaagccatt cgccttaac cgcctttcag accgagcaaa tacaagattc ggagcattcc      360
gggaagatgg ttgcgaaacg ccagttcaga atcggcgaca tagcgggcca acatacatct      420
tttgacaagc ttcccgaagg cggcagggcg acatatcgcg ggacggcggt cggttcagac      480
gatgccggcg gaaaactgac ctacaccata gatttcgccc ccaagcaggg aaacggcaaa      540
atcgaacatt tgaaatcgcc agaactcaat gtcgacctgg ccgccgccga tatcaagccg      600
gatggaaaac gccatgccgt catcagcggg tccgtccttt acaaccaagc cgagaaaggc      660
agttactccc tcggtatctt tggcggaaaa gccaggaag ttgccggcag cgcggaagtg      720
aaaaccgtaa acggcatacg ccatatcggc cttgccgccg agcaataa      768

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<210> 194
<211> 255
<212> PRT
<213> Neisseria meningitidis

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<400> 194

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```

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10           15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln
          20           25           30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35           40           45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50           55           60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65           70           75           80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
          85           90           95

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln Thr Glu
          100          105          110

Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln
          115          120          125

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179

Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
 130 135 140

Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp
 180 185 190

Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val Ile
 195 200 205

Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu
 210 215 220

Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240

Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 195

<211> 771

<212> DNA

<213> *Neisseria meningitidis*

<400> 195

tgccgatcca gcgaggggg tgggtgcgcc gccgacatcg gtgcggggct tgccgatgca	60
ctaaccgcac cgctcgacca taaagacaaa ggtttgagct ctttgacgct ggatcagtcc	120
gtcaggaaaa acgagaaaact gaagctggcg gcacaaggtg cggaaaaaac ttatggaaac	180
ggtgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgttt cgactttatc	240
cgccaaatcg aagtggacgg gcagctcatt accttggaga gtggagagtt ccaagtatac	300
aaacaaagcc attccgcctt aaccgccttt cagaccgagc aaatacaaga ttcggagcat	360
tccgggaaga tggttgcgaa acgccagttc agaatcgggc acatagcggg cgaacataca	420
tcttttgaca agcttcccga aggcggcagg gcgacatatc gcgggacggc gttcggttca	480
gacgatgccg gcggaaaact gacctacacc atagatttcg ccgccaagca gggaaacggc	540
aaaatcgaac atttgaaatc gccagaactc aatgtcgacc tggccgccgc cgatatcaag	600

180

ccggatggaa aacgccatgc cgtcacacgc ggttcctgcc tttaacaacca agccgagaaa 660
 ggcagttact ccctcggtat ctttggcgga aaagcccagg aagttgccgg cagcgcgga 720
 gtgaaaaccg taaacggcat acgcatatc ggccttgccg ccaagcaata a 771

<210> 196
 <211> 256
 <212> PRT
 <213> Neisseria meningitidis

<400> 196

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu
 20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
 35 40 45

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
 85 90 95

Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln Thr
 100 105 110

Glu Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg
 115 120 125

Gln Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys
 130 135 140

Leu Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser
 145 150 155 160

Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys
 165 170 175

181

Gln Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val
 180 185 190

Asp Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val
 195 200 205

Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser
 210 215 220

Leu Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu
 225 230 235 240

Val Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 197

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 197

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atgagcagcg gagggggtgg tgtcgccgcc gacatcggtg cggggcttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaggt ttgcagtctt tgacgctgga tcagtcctgc      120
aggaaaaacg agaaactgaa gctggcgggc caaggtgcgg aaaaaactta tggaaacggt      180
gacagcctca atacggggcaa attgaagaac gacaaggtca gccgtttcga ctttatccgc      240
caaatcgaag tggacgggca gctcattacc ttggagagtg gagagttcca agtatacaaa      300
caaagccatt ccgccttaac cgcttttcag accgagcaaa tacaagattc ggagcattcc      360
gggaagatgg ttgcgaaacg ccagttcaga atcggcgaca tagcgggcca acatacatct      420
tttgacaagc ttcccgaagg cggcagggcg acatatcgcg ggacggcggt cggttcagac      480
gatgccggcg gaaaactgac ctacaccata gatttcgccg ccaagcaggg aaacggcaaa      540
atcgaacatt tgaaatcgcc agaactcaat gtcgacctgg ccgccgccga tatcaagccg      600
gatggaaaac gccatgccgt catcagcggg tccgtccttt acaaccaagc cgagaaaggc      660
agttactccc tcggtatctt tggcggaaaa gccaggaag ttgccggcag cgcggaagtg      720
aaaaccgtaa acggcatacg ccatatcggc cttgccgccg agcaataa      768

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<210> 198

<211> 255

182

<212> PRT

<213> Neisseria meningitidis

<400> 198

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln Thr Glu
 100 105 110

Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln
 115 120 125

Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
 130 135 140

Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp
 180 185 190

Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val Ile
 195 200 205

183

Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu
 210 215 220

Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240

Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 199

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 199

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tgcagcagcg gagggggtgg tgtcgccgcc gacatcggtg cggggcttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaggt ttgcagtctt tgacgctgga tcagtccgtc      120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggt      180
gacagcctca atacgggcaa attgaagaac gacaaggtca gccgtttcga ctttatccgc      240
caaatcgaag tggacgggca gctcattacc ttggagagtg gagagttcca agtatacaaa      300
caaagccatt ccgccttaac cgcctttcag accgagcaaa tacaagattc ggagcattcc      360
gggaagatgg ttgcgaaacg ccagttcaga atcggcgaca tagcggggcg acatacatct      420
tttgacaagc ttcccgaagg cggcagggcg acatatcgcg ggacggcggt cggttcagac      480
gatgccggcg gaaaactgac ctacaccata gatttcgccg ccaagcaggg aaacggcaaa      540
atcgaacatt tgaaatcgcc agaactcaat gtcgacctgg ccgccgccga tatcaagccg      600
gatggaaaac gccatgccgt catcagcggg tccgtccttt acaaccaagc cgagaaaggc      660
agttactccc tcggtatctt tggcggaaaa gccaggaag ttgccggcag cgcggaagtg      720
aaaaccgtaa acggcatacg ccatatcggc cttgccgccca agcaataa      768

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<210> 200

<211> 255

<212> PRT

<213> Neisseria meningitidis

<400> 200

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln

30

Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
245 250 255

185

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<210> 201
<211> 771
<212> DNA
<213> Neisseria meningitidis

<400> 201
tgcggatcca gcggaggggg tggtgtcgcc gccgacatcg gtgcgggggt tgccgatgca      60
ctaaccgcac cgctcgacca taaagacaaa ggtttgcagt ctttgacgct ggatcagtc      120
gtcaggaaaa acgagaaaact gaagctggcg gcacaagggt cggaaaaaac ttatggaaac      180
ggtgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgttt cgactttatc      240
cgccaaatcg aagtggacgg gcagctcatt accttggaga gtggagagtt ccaagtatac      300
aaacaaagcc attccgcctt aaccgccttt cagaccgagc aaatacaaga ttcggagcat      360
tccgggaaga tggttgcgaa acgccagttc agaatcggcg acatagcggg cgaacataca      420
tcttttgaca agcttcccgga aggcggcagg gcgacatata gcgggacggc gttcggttca      480
gacgatgccg gcggaaaact gacctacacc atagatttcg ccgccaagca gggaaacggc      540
aaaatcgaac atttgaaatc gccagaactc aatgtcgacc tggccgccgc cgatatcaag      600
ccggatggaa aacgccatgc cgtcatcagc ggttccgtcc ttacaacca agccgagaaa      660
ggcagttact ccctcggtat ctttggcgga aaagcccagg aagttgccgg cagcgcggaa      720
gtgaaaaccg taaacggcat acgcatatc ggccttgccg ccaagcaata a              771

```

```

<210> 202
<211> 256
<212> PRT
<213> Neisseria meningitidis

<400> 202

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
1          5          10          15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu
20          25          30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
35          40          45

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
50          55          60

```


186

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
65 70 75 80

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
85 90 95

Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln Thr
100 105 110

Glu Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg
115 120 125

Gln Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys
130 135 140

Leu Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser
145 150 155 160

Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys
165 170 175

Gln Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val
180 185 190

Asp Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val
195 200 205

Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser
210 215 220

Leu Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu
225 230 235 240

Val Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
245 250 255

<210> 203

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 203

atgagcagcg gagggggtgg tgtcgccgcc gacatcggtg cggggcttgc cgatgcacta

60

187

```

accgcaccgc tcgaccataa agacaaaggt ttgcagtctt tgacgctgga tcagtccgtc   120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggt   180
gacagcctca atacgggcaa attgaagaac gacaaggtca gccgtttcga ctttatccgc   240
caaatcgaag tggacgggca gctcattacc ttggagagtg gagagttcca agtatacaaaa   300
caaagccatt ccgccttaac cgcctttcag accgagcaaa tacaagattc ggagcattcc   360
gggaagatgg ttgcgaaacg ccagttcaga atcggcgaca tagcgggcca acatacatct   420
tttgacaagc ttcccgaagg cggcagggcg acatatcgcg ggacggcggt cggttcagac   480
gatgccggcg gaaaactgac ctacaccata gatttcgccg ccaagcaggg aaacggcaaa   540
atcgaacatt tgaaatcgcc agaactcaat gtcgacctgg ccgccgccga tatcaagccg   600
gatggaaaac gccatgccgt catcagcggg tccgtccttt acaaccaagc cgagaaaggc   660
agttactccc tcggtatctt tggcggaaaa gccaggaag ttgccggcag cgcggaagtg   720
aaaaccgtaa acggcatacg ccatatcggc cttgccgcca agcaataa               768

```

```

<210> 204
<211> 255
<212> PRT
<213> Neisseria meningitidis

```

```

<400> 204

```

```

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10          15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln
          20          25          30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35          40          45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50          55          60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65          70          75          80

```

```

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
          85          90          95

```

```

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln Thr Glu

```


188

100 105 110
 Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln
 115 120 125
 Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
 130 135 140
 Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160
 Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175
 Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp
 180 185 190
 Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val Ile
 195 200 205
 Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu
 210 215 220
 Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240
 Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 205

<211> 768

<212> DNA

<213> *Neisseria meningitidis*

<400> 205

tgcagcagcg gagggggtgg tgctgccgcc gacatcgggtg cggggcttgc cgatgcacta	60
accgcaccgc tcgaccataa agacaaaagggt ttgcagtctt tgacgctgga tcagtccgtc	120
aggaaaaacg agaaactgaa gctggcggca caaggtgctg aaaaaactta tggaaacggt	180
gacagcctca atacgggcaa attgaagaac gacaagggtca gccgtttcga ctttatccgc	240
caaatcgaag tggacgggca gctcattacc ttggagagtg gagagttcca agtatacaaa	300
caaagccatt ccgccttaac cgcctttcag accgagcaaa tacaagattc ggagcattcc	360

189

```

gggaagatgg ttgcgaaacg ccagttcaga atcggcgaca tagcgggcga acatacatct      420
tttgacaagc ttcccgaagg cggcagggcg acatatcgcg ggacggcggt cggttcagac      480
gatgccggcg gaaaactgac ctacaccata gatttcgccg ccaagcaggg aaacggcaaa      540
atcgaacatt tgaaatcgcc agaactcaat gtcgacctgg ccgccgccga tatcaagccg      600
gatggaaaac gccatgccgt catcagcggg tccgtccttt acaaccaagc cgagaaaggc      660
agttactccc tcggtatctt tggcggaaaa gcccgaggaag ttgccggcag cgcggaagtg      720
aaaaccgtaa acggcatacg ccatatcggc cttgccgcca agcaataa                      768

```

<210> 206

<211> 255

<212> PRT

<213> *Neisseria meningitidis*

<400> 206

```

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10           15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln
          20           25           30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35           40           45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50           55           60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65           70           75           80

```

```

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
          85           90           95

```

```

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln Thr Glu
          100          105          110

```

```

Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln
          115          120          125

```

```

Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
          130          135          140

```


190

Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp
 180 185 190

Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val Ile
 195 200 205

Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu
 210 215 220

Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240

Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 207

<211> 771

<212> DNA

<213> Neisseria meningitidis

<400> 207

tgcggtatcca gcgagggggg tgggtgtcgcc gccgacatcg gtgcgggggct tgccgatgca	60
ctaaccgcac cgctcgacca taaagacaaa ggtttgcagt ctttgacgct ggatcagtc	120
gtcaggaaaa acgagaaact gaagctggcg gcacaagggtg cggaaaaaac ttatggaaac	180
ggtgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgttt cgactttatc	240
cgccaaatcg aagtggacgg gcagctcatt accttggaga gtggagagtt ccaagtatac	300
aaacaaagcc attccgcctt aaccgccttt cagaccgagc aaatacaaga ttcggagcat	360
tccgggaaga tggttgcgaa acgccagttc agaatcggcg acatagcggg cgaacataca	420
tcttttgaca agcttcccga aggcggcagg gcgacatatc gcgggacggc gttcggttca	480
gacgatgccg gcggaaaact gacctacacc atagatttcg ccgccaagca gggaaacggc	540
aaaatcgaac atttgaaatc gccagaactc aatgtcgacc tggccgccgc cgatatcaag	600
ccggatggaa aacgccatgc cgtcatcagc gggttcgtcc tttaacaacca agccgagaaa	660

191

ggcagttact ccctcggtat ctttggcgga aaagcccagg aagttgccgg cagcgcgga 720

gtgaaaaccg taaacggcat acgccatatc ggccttgccg ccaagcaata a 771

<210> 208

<211> 256

<212> PRT

<213> Neisseria meningitidis

<400> 208

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu
20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
35 40 45

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
50 55 60

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
65 70 75 80

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
85 90 95

Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln Thr
100 105 110

Glu Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg
115 120 125

Gln Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys
130 135 140

Leu Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser
145 150 155 160

Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys
165 170 175

Gln Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val

192

180	185	190
Asp Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val		
195	200	205
Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser		
210	215	220
Leu Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu		
225	230	235 240
Val Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln		
245	250	255

<210> 209

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 209

atgagcagcg gagggggtgg tgtcgccgcc gacatcgggtg cggggcttgc cgatgcacta	60
accgcaccgc tcgaccataa agacaaaggt ttgcagtctt tgacgctgga tcagtccgtc	120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggt	180
gacagcctca atacgggcaa attgaagaac gacaaggtca gccgtttcga ctttatccgc	240
caaatcgaag tggacgggca gctcattacc ttggagagtg gagagttcca agtatacaaa	300
caaagccatt ccgccttaac cgcctttcag accgagcaaa tacaagattc ggagcattcc	360
gggaagatgg ttgcgaaacg ccagttcaga atcggcgaca tagcgggcca acatacatct	420
tttgacaagc ttcccgaagg cggcagggcg acatatcgcg ggacggcggt cggttcagac	480
gatgccggcg gaaaactgac ctacaccata gatattcgccg ccaagcaggg aaacggcaaa	540
atcgaacatt tgaaatcgcc agaactcaat gtcgacctgg ccgccgccga tatcaagccg	600
gatggaaaac gccatgccgt catcagcgggt tccgtccttt acaaccaagc cgagaaaggc	660
agttactccc tcggtatctt tggcggaaaa gcccaggaag ttgccggcag cgcggaagtg	720
aaaaccgtaa acggcatacg ccatatcggc cttgccgccga agcaataa	768

<210> 210

<211> 255

<212> PRT

<213> Neisseria meningitidis

193

<400> 210

```

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1           5           10           15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln
 20           25           30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35           40           45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50           55           60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65           70           75           80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85           90           95

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln Thr Glu
100           105           110

Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln
115           120           125

Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
130           135           140

Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
145           150           155           160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
165           170           175

Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp
180           185           190

Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val Ile
195           200           205

Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu
210           215           220

```


194

Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240

Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 211

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 211

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tgcagcagcg gagggggtgg tgtcgccgcc gacatcggtg cggggcttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaggt ttgcagtctt tgacgctgga tcagtccgtc      120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggt      180
gacagcctca atacgggcaa attgaagaac gacaaggtca gccgtttcga ctttatccgc      240
caaatcgaag tggacgggca gctcattacc ttggagagtg gagagttcca agtatacaaa      300
caaagccatt ccgccttaac cgcctttcag accgagcaaa tacaagattc ggagcattcc      360
gggaagatgg ttgcgaaacg ccagttcaga atcggcgaca tagcgggcga acatacatct      420
tttgacaagc ttcccgaagg cggcagggcg acatatcgcg ggacggcggt cggttcagac      480
gatgccggcg gaaaactgac ctacaccata gatttcgccg ccaagcaggg aaacggcaaa      540
atcgaacatt tgaaatcgcc agaactcaat gtcgacctgg ccgccgccga tatcaagccg      600
gatggaaaac gccatgccgt catcagcggg tccgtccttt acaaccaagc cgagaaaggc      660
agttactccc tcggtatctt tggcggaaaa gccaggaag ttgccggcag cgcggaagtg      720
aaaaccgtaa acggcatacg ccatatcggt cttgccgcca agcagtaa      768

```

<210> 212

<211> 255

<212> PRT

<213> Neisseria meningitidis

<400> 212

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln
 20 25 30

195

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln Thr Glu
 100 105 110

Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln
 115 120 125

Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
 130 135 140

Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp
 180 185 190

Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val Ile
 195 200 205

Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu
 210 215 220

Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240

Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 213

196

<211> 771
 <212> DNA
 <213> *Neisseria meningitidis*

<400> 213
 tgcggatcca gcggaggggg tgggtgtcgcc gccgacatcg gtgcggggct tgccgatgca 60
 ctaaccgcac cgctcgacca taaagacaaa ggtttgcagt ctttgacgct ggatcagtc 120
 gtcaggaaaa acgagaaact gaagctggcg gcacaagggtg cggaaaaaac ttatggaaac 180
 ggtgacagcc tcaatacggg caaattgaag aacgacaagg tcagccggtt cgactttatc 240
 cgccaaatcg aagtggacgg gcagctcatt accttggaga gtggagagtt ccaagtatac 300
 aaacaaagcc attccgcctt aaccgccttt cagaccgagc aaatacaaga ttcgagagcat 360
 tccgggaaga tggttgcgaa acgccagttc agaatcggcg acatagcggg cgaacatata 420
 tcttttgaca agcttcccgga aggcggcagg gcgacatatc gcgggacggc gttcgggttca 480
 gacgatgccg gcggaaaact gacctacacc atagatttcg ccgccaagca gggaaacggc 540
 aaaatcgaac atttgaaatc gccagaactc aatgtcgacc tggccgccgc cgatatcaag 600
 ccggatggaa aacgccatgc cgtcatcagc ggttccgtcc ttacaacca agccgagaaa 660
 ggcagttact ccctcggtat ctttggcgga aaagcccagg aagttgccgg cagcgcgga 720
 gtgaaaaccg taaacggcat acgcatatc ggtcttgccg ccaagcagta a 771

<210> 214
 <211> 256
 <212> PRT
 <213> *Neisseria meningitidis*

<400> 214
 Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15
 Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu
 20 25 30
 Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
 35 40 45
 Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60
 Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80

197

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
85 90 95

Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln Thr
100 105 110

Glu Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg
115 120 125

Gln Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys
130 135 140

Leu Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser
145 150 155 160

Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys
165 170 175

Gln Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val
180 185 190

Asp Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val
195 200 205

Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser
210 215 220

Leu Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu
225 230 235 240

Val Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
245 250 255

<210> 215

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 215

atgagcagcg gagggggtgg tgtcgccgcc gacatcggtg cggggcttgc cgatgcacta 60

accgcaccgc tcgaccataa agacaaaggt ttgcagtctt tgacgctgga tcagtccgtc 120

aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggt 180

198

```

gacagcctca atacgggcaa attgaagaac gacaagggtca gccgtttcga ctttatccgc      240
caaatcgaag tggacgggca gctcattacc ttggagagtg gagagttcca agtatacaaaa      300
caaagccatt ccgccttaac cgcctttcag accgagcaaaa tacaagattc ggagcattcc      360
gggaagatgg ttgcgaaacg ccagttcaga atcggcgaca tagcgggcca acatacatct      420
tttgacaagc ttcccgaagg cggcagggcg acatatcgcg ggacggcggt cggttcagac      480
gatgccggcg gaaaactgac ctacaccata gatttcgccc ccaagcaggg aaacggcaaaa      540
atcgaacatt tgaaatcgcc agaactcaat gtcgacctgg ccgccgccga tatcaagccg      600
gatggaaaac gccatgccgt catcagcggg tccgtccttt acaaccaagc cgagaaaaggc      660
agttactccc tcggtatctt tggcggaaaa gcccgaggaag ttgccggcag cgcggaagtg      720
aaaaccgtaa acggcatacg ccatatcggt cttgcgcgcca agcagtaa                    768

```

```

<210> 216
<211> 255
<212> PRT
<213> Neisseria meningitidis

```

```

<400> 216

```

```

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10           15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln
          20           25           30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35           40           45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50           55           60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65           70           75           80

```

```

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
          85           90           95

```

```

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln Thr Glu
          100          105          110

```


199

Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln
 115 120 125

Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
 130 135 140

Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp
 180 185 190

Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val Ile
 195 200 205

Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu
 210 215 220

Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240

Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 217

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 217

tgcagcagcg gagggggcgg tgtcgccgcc gacatcggtg cggggcttgc cgatgcacta	60
accgcaccgc tcgaccataa agacaaaggt ttgcagtctt tgacgctgga tcagtccgtc	120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc	180
gacagcctca atacgggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt	240
caaatcgaag tggacaggca gctcattacc ttggagagcg gagagttcca agtgtacaaa	300
caaagccatt ccgccttaac cgcccttcag accgagcaag tacaagactc ggagcattcc	360
gggaagatgg ttgcgaaacg tcagttcaga atcggcgaca tagcgggtga acatacatct	420
tttgacaagc ttcccgaagg cggcagggcg acatatcgcg ggacggcggtt cggttcagac	480

200

```

gatgccggcg gaaaactgat ttacaccata gatttcgccg ctaagcaggg acacggtaaa      540
atcgaacatt tgaaatcgcc agaactcaat gtcgacctgg ccgccgccga tatcaagccg      600
gatgaaaaaac accatgccgt catcagcggg tccgtccttt acaaccaagc cgagaaaggc      660
agttactccc tcggtatctt tggcggaaaa gcccgaggaag ttgccggcag cgcggaagtg      720
aaaaccgtaa acggtatacg ccatatcggc cttgccgcca agcaataa                    768

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<210> 218

<211> 255

<212> PRT

<213> Neisseria meningitidis

<400> 218

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Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10           15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln
          20           25           30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
      35           40           45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
      50           55           60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65           70           75           80

```

```

Gln Ile Glu Val Asp Arg Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
          85           90           95

```

```

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu
      100           105           110

```

```

Gln Val Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln
      115           120           125

```

```

Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
      130           135           140

```

```

Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
145           150           155           160

```


201

Asp Ala Gly Gly Lys Leu Ile Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp
 180 185 190

Leu Ala Ala Ala Asp Ile Lys Pro Asp Glu Lys His His Ala Val Ile
 195 200 205

Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu
 210 215 220

Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240

Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 219

<211> 771

<212> DNA

<213> *Neisseria meningitidis*

<400> 219

tgccgatcca gcggaggggg cggtgtcgcc gccgacatcg gtgcgggggct tgccgatgca	60
ctaaccgcac cgctcgacca taaagacaaa ggtttgcagt ctttgacgct ggatcagtcc	120
gtcaggaaaa acgagaaact gaagctggcg gcacaagggt cggaaaaaac ttatggaaac	180
ggcgacagcc tcaatacggg caaattgaag aacgacaagg tcagccgctt cgactttatc	240
cgtcaaatcg aagtggacag gcagctcatt accttggaga gcggagagtt ccaagtgtac	300
aaacaaagcc attccgcctt aaccgccctt cagaccgagc aagtacaaga ctcggagcat	360
tccgggaaga tggttgcgaa acgtcagttc agaatcggcg acatagcggg tgaacataca	420
tcttttgaca agcttcccga aggcggcagg gcgacatatc gcgggacggc gttcggttca	480
gacgatgccg gcggaaaact gatttacacc atagatttcg ccgctaagca gggacacggg	540
aaaatcgaac atttgaaatc gccagaactc aatgtcgacc tggccgccgc cgatatcaag	600
ccggatgaaa aacaccatgc cgtcatcagc ggttccgtcc tttacaacca agccgagaaa	660
ggcagttact ccctcggtat ctttggcgga aaagcccagg aagttgccgg cagcgcggaa	720
gtgaaaaccg taaacggtat acgccatatc ggcccttgccg ccaagcaata a	771

202

<210> 220
 <211> 256
 <212> PRT
 <213> Neisseria meningitidis

<400> 220

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu
 20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
 35 40 45

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80

Arg Gln Ile Glu Val Asp Arg Gln Leu Ile Thr Leu Glu Ser Gly Glu
 85 90 95

Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr
 100 105 110

Glu Gln Val Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg
 115 120 125

Gln Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys
 130 135 140

Leu Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser
 145 150 155 160

Asp Asp Ala Gly Gly Lys Leu Ile Tyr Thr Ile Asp Phe Ala Ala Lys
 165 170 175

Gln Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val
 180 185 190

203

Asp Leu Ala Ala Ala Asp Ile Lys Pro Asp Glu Lys His His Ala Val
 195 200 205

Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser
 210 215 220

Leu Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu
 225 230 235 240

Val Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 221

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 221

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atgagcagcg gagggggcgg tgcgccgcc gacatcggtg cggggcttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaggt ttgcagtctt tgacgctgga tcagtcgcgc      120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc      180
gacagcctca atacgggcaa attgaagaac gacaaggcca gccgcttcga ctttatccgt      240
caaatcgaag tggacaggca gctcattacc ttggagagcg gagagttcca agtgtacaaa      300
caaagccatt ccgccttaac cgcccttcag accgagcaag tacaagactc ggagcattcc      360
gggaagatgg ttgcgaaacg tcagttcaga atcggcgaca tagcgggtga acatacatct      420
tttgacaagc ttcccgaagg cggcagggcg acatatcgcg ggacggcggt cggttcagac      480
gatgccggcg gaaaactgat ttacaccata gatttcgccg ctaagcaggg acacggtaaa      540
atcgaacatt tgaaatcgcc agaactcaat gtcgacctgg ccgccgccga tatcaagccg      600
gatgaaaaac accatgccgt catcagcggc tccgtccttt acaaccaagc cgagaaaggc      660
agttactccc tcggtatctt tggcggaaaa gccaggaag ttgccggcag cgcggaagtg      720
aaaaccgtaa acggtatacg ccatatcggc cttgccgcca agcaataa      768

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<210> 222

<211> 255

<212> PRT

<213> Neisseria meningitidis

<400> 222

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu

204

1	5	10	15
Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln	20	25	30
Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu	35	40	45
Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn	50	55	60
Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg	65	70	75
Gln Ile Glu Val Asp Arg Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe	85	90	95
Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu	100	105	110
Gln Val Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln	115	120	125
Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu	130	135	140
Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp	145	150	155
Asp Ala Gly Gly Lys Leu Ile Tyr Thr Ile Asp Phe Ala Ala Lys Gln	165	170	175
Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp	180	185	190
Leu Ala Ala Ala Asp Ile Lys Pro Asp Glu Lys His His Ala Val Ile	195	200	205
Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu	210	215	220
Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu Val	225	230	235
			240

Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
245 250 255

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<210> 223
<211> 768
<212> DNA
<213> Neisseria meningitidis
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[illegible]

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<210> 224
<211> 255
<212> PRT
<213> Neisseria meningitidis
```

<400> 224

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln
20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
35 40 45

206

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Lys Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu
 100 105 110

Gln Val Gln Asp Ser Glu Asp Ser Gly Lys Met Val Ala Lys Arg Gln
 115 120 125

Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
 130 135 140

Pro Lys Gly Gly Ser Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Glu
 180 185 190

Leu Ala Thr Ala Tyr Ile Lys Pro Asp Glu Lys Arg His Ala Val Ile
 195 200 205

Ser Gly Ser Val Leu Tyr Asn Gln Asp Glu Lys Gly Ser Tyr Ser Leu
 210 215 220

Gly Ile Phe Gly Gly Gln Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240

Glu Thr Ala Asn Gly Ile His His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 225

<211> 771

<212> DNA

<213> Neisseria meningitidis

207

<400> 225
 tgcggatcca gcggaggggg cggtgtcgcc gccgacatcg gtgcggggct tgccgatgca 60
 ctaaccgcac cgctcgacca taaagacaaa ggtttgcaagt ctttaacgct ggatcagtc 120
 gtcaggaaaa acgagaaact gaagctggcg gcacaagggt cggaaaaaac ttatggaaac 180
 ggcgacagcc ttaatacggg caaattgaag aacgacaagg tcagccgctt cgactttatc 240
 cgtcaaactc aagtggacgg gaagctcatt accttgaga gcggagagtt ccaagtgtac 300
 aaacaaagcc attccgcctt aaccgcctt cagaccgagc aagtacaaga ctcgaggat 360
 tccgggaaga tggttgcga acgccagttc agaatcgcg acatagcggg cgaacataca 420
 tcttttgaca agcttcccaa aggcggcagt gcgacatata gcgggacggc gttcggttca 480
 gacgatgctg gcggaaaact gacctatact atagatttcg ccgccaagca gggacacggc 540
 aaaatcgaac atttgaaatc gccggaactc aatgtcgagc ttgccaccgc ctatatcaag 600
 ccggatgaaa aacgccatgc cgttatcagc ggttcgctc ttacaacca agacgagaaa 660
 ggcagttact ccctcggtat ctttggcggg caagcccagg aagttgcccg cagcgcgga 720
 gtggaaaccg caaacggcat acaccatata ggtcttgccg ccaagcagta a 771

<210> 226
 <211> 256
 <212> PRT
 <213> Neisseria meningitidis

<400> 226

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu
 20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
 35 40 45

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80

Arg Gln Ile Glu Val Asp Gly Lys Leu Ile Thr Leu Glu Ser Gly Glu

208

	85		90		95										
Phe	Gln	Val	Tyr	Lys	Gln	Ser	His	Ser	Ala	Leu	Thr	Ala	Leu	Gln	Thr
	100							105					110		
Glu	Gln	Val	Gln	Asp	Ser	Glu	Asp	Ser	Gly	Lys	Met	Val	Ala	Lys	Arg
	115						120					125			
Gln	Phe	Arg	Ile	Gly	Asp	Ile	Ala	Gly	Glu	His	Thr	Ser	Phe	Asp	Lys
	130					135					140				
Leu	Pro	Lys	Gly	Gly	Ser	Ala	Thr	Tyr	Arg	Gly	Thr	Ala	Phe	Gly	Ser
145					150					155					160
Asp	Asp	Ala	Gly	Gly	Lys	Leu	Thr	Tyr	Thr	Ile	Asp	Phe	Ala	Ala	Lys
			165						170					175	
Gln	Gly	His	Gly	Lys	Ile	Glu	His	Leu	Lys	Ser	Pro	Glu	Leu	Asn	Val
		180						185					190		
Glu	Leu	Ala	Thr	Ala	Tyr	Ile	Lys	Pro	Asp	Glu	Lys	Arg	His	Ala	Val
	195						200					205			
Ile	Ser	Gly	Ser	Val	Leu	Tyr	Asn	Gln	Asp	Glu	Lys	Gly	Ser	Tyr	Ser
	210					215					220				
Leu	Gly	Ile	Phe	Gly	Gly	Gln	Ala	Gln	Glu	Val	Ala	Gly	Ser	Ala	Glu
225					230					235					240
Val	Glu	Thr	Ala	Asn	Gly	Ile	His	His	Ile	Gly	Leu	Ala	Ala	Lys	Gln
			245						250					255	

<210> 227

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 227

atgagcagcg gagggggcgg tgctcgccgcc gacatcgggtg cggggccttgc cgatgcacta	60
accgcaccgc tcgaccataa agacaaaggt ttgcagtctt taacgctgga tcagtccgtc	120
aggaaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc	180
gacagcctta atacgggcaa attgaagaac gacaagggtca gccgcttcga ctttatccgt	240

209

```

caaatcgaag tggacgggaa gctcattacc ttggagagcg gagagttcca agtgtacaaa    300
caaagccatt ccgccttaac cgcccttcag accgagcaag tacaagactc ggaggattcc    360
gggaagatgg ttgcgaaacg ccagttcaga atcggcgaca tagcgggcga acatacatct    420
tttgacaagc ttcccaaagg cggcagtgcg acatatcgcg ggacggcggt cggttcagac    480
gatgctggcg gaaaactgac ctatactata gatttcgccg ccaagcaggg acacggcaaa    540
atcgaacatt tgaaatcgcc cgaactcaat gtcgagcttg ccaccgccta tatcaagccg    600
gatgaaaaac gccatgccgt tatcagcggg tccgtccttt acaaccaaga cgagaaaggc    660
agttactccc tcggtatctt tggcgggcaa gccaggaag ttgccggcag cgcggaagtg    720
gaaaccgcaa acggcataca ccatatcggt cttgccgcca agcagtaa                    768

```

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<210> 228
<211> 255
<212> PRT
<213> Neisseria meningitidis

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```

<400> 228

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```

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10           15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln
          20           25           30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35           40           45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50           55           60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65           70           75           80

```

```

Gln Ile Glu Val Asp Gly Lys Leu Ile Thr Leu Glu Ser Gly Glu Phe
          85           90           95

```

```

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu
          100          105          110

```

```

Gln Val Gln Asp Ser Glu Asp Ser Gly Lys Met Val Ala Lys Arg Gln
          115          120          125

```


210

Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
 130 135 140

Pro Lys Gly Gly Ser Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Glu
 180 185 190

Leu Ala Thr Ala Tyr Ile Lys Pro Asp Glu Lys Arg His Ala Val Ile
 195 200 205

Ser Gly Ser Val Leu Tyr Asn Gln Asp Glu Lys Gly Ser Tyr Ser Leu
 210 215 220

Gly Ile Phe Gly Gly Gln Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240

Glu Thr Ala Asn Gly Ile His His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 229

<211> 768

<212> DNA

<213> *Neisseria meningitidis*

<400> 229

tgcagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta	60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgctc	120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc	180
gacagcctta atacgggcaa attgaagaac gacaaggtca gccgtttcga ctttatccgt	240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca agtgtacaaa	300
caaagccatt ccgccttaac cgcccttcag accgagcaag aacaagatcc agagcattcc	360
gggaagatgg ttgcgaaacg ccggttcaaa atcggcgaca tagcgggcca acatacatct	420
tttgacaagc ttcccaaaga cgatcatggcg acatatcgcg ggacggcggt cggttcagac	480
gatgccggcg gaaaactgac ctatactata gattttgctg ccaaacaggg acacggcaaa	540

211

atcgaacatt tgaaatcgcc cgaactcaat gtcgagcttg ccaccgccta tatcaagccg 600
gatgaaaaac accatgccgt catcagcggg tccgtccttt acaatcaaga cgagaaaggc 660
agttactccc tcggtatctt tggcgggcaa gcccaggaag ttgccggcag cgcggaagtg 720
gaaaccgcaa acggcatata ccatatcggt cttgccgcca agcaataa 768

<210> 230
<211> 255
<212> PRT
<213> Neisseria meningitidis
<400> 230

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
85 90 95

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu
100 105 110

Gln Glu Gln Asp Pro Glu His Ser Gly Lys Met Val Ala Lys Arg Arg
115 120 125

Phe Lys Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
130 135 140

Pro Lys Asp Val Met Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln

212

	165		170		175
Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Glu					
	180		185		190
Leu Ala Thr Ala Tyr Ile Lys Pro Asp Glu Lys His His Ala Val Ile					
	195		200		205
Ser Gly Ser Val Leu Tyr Asn Gln Asp Glu Lys Gly Ser Tyr Ser Leu					
	210		215		220
Gly Ile Phe Gly Gly Gln Ala Gln Glu Val Ala Gly Ser Ala Glu Val					
	225		230		235
					240
Glu Thr Ala Asn Gly Ile His His Ile Gly Leu Ala Ala Lys Gln					
	245		250		255

<210> 231
 <211> 771
 <212> DNA
 <213> Neisseria meningitidis

<400> 231
 tgcggatcca gcggaggcgg cgggtgtcgcc gccgacatcg gcgcggggct tgccgatgca 60
 ctaaccgcac cgctcgacca taaagacaaa agtttgcagt ctttgacgct ggatcagtcc 120
 gtcaggaaaa acgagaaaact gaagctggcg gcacaagggtg cggaaaaaac ttatggaaac 180
 ggcgacagcc ttaatacggg caaattgaag aacgacaagg tcagccgttt cgactttatc 240
 cgtcaaactg aagtggacgg gcagctcatt accttggaga gcggagagtt ccaagtgtac 300
 aaacaaagcc attccgcctt aaccgccctt cagaccgagc aagaacaaga tccagagcat 360
 tccgggaaga tggttgcaa acgccggttc aaaatcggcg acatagcggg cgaacataca 420
 tcttttgaca agcttcccaa agacgtcatg gcgacatc gcgggacggc gttcggttca 480
 gacgatgccg gcggaaaact gacctatact atagattttg ctgccaaaca gggacacggc 540
 aaaatcgaac atttgaaatc gcccgaaactc aatgtcgagc ttgccaccgc ctatatcaag 600
 ccggatgaaa aacaccatgc cgtcatcagc ggttccgtcc ttacaatca agacgagaaa 660
 ggcagttact ccctcggat ctttggcggg caagcccagg aagttgccgg cagcgcggaa 720
 gtggaaaccg caaacggcat acaccatc ggtcttgccg ccaagcaata a 771

<210> 232

213

<211> 256

<212> PRT

<213> Neisseria meningitidis

<400> 232

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
 20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
 35 40 45

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
 85 90 95

Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr
 100 105 110

Glu Gln Glu Gln Asp Pro Glu His Ser Gly Lys Met Val Ala Lys Arg
 115 120 125

Arg Phe Lys Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys
 130 135 140

Leu Pro Lys Asp Val Met Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser
 145 150 155 160

Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys
 165 170 175

Gln Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val
 180 185 190

Glu Leu Ala Thr Ala Tyr Ile Lys Pro Asp Glu Lys His His Ala Val
 195 200 205

214

Ile Ser Gly Ser Val Leu Tyr Asn Gln Asp Glu Lys Gly Ser Tyr Ser
 210 215 220

Leu Gly Ile Phe Gly Gly Gln Ala Gln Glu Val Ala Gly Ser Ala Glu
 225 230 235 240

Val Glu Thr Ala Asn Gly Ile His His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 233

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 233

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atgagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc      120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc      180
gacagcctta atacgggcaa attgaagaac gacaaggcca gccgtttcga ctttatccgt      240
caaatcgaag tggacgggca gtcattacc ttggagagcg gagagttcca agtgtacaaa      300
caaagccatt ccgccttaac cgcccttcag accgagcaag aacaagatcc agagcattcc      360
gggaagatgg ttgcgaaacg ccggttcaaa atcggcgaca tagcgggcca acatacatct      420
tttgacaagc ttcccaaaga cgtcatggcg acatatcgcg ggacggcggt cggttcagac      480
gatgccggcg gaaaactgac ctatactata gattttgctg ccaaacaggg acacggcaaa      540
atcgaacatt tgaaatcgcc cgaactcaat gtcgagcttg ccaccgccta tatcaagccg      600
gatgaaaaac accatgccgt catcagcggg tccgtccttt acaatcaaga cgagaaaggc      660
agttactccc tcggtatctt tggcgggcaa gccaggaag ttgccggcag cgcggaagtg      720
gaaaccgcaa acggcataca ccatatcggt cttgccgcca agcaataa      768

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<210> 234

<211> 255

<212> PRT

<213> Neisseria meningitidis

<400> 234

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

215

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu
 100 105 110

Gln Glu Gln Asp Pro Glu His Ser Gly Lys Met Val Ala Lys Arg Arg
 115 120 125

Phe Lys Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
 130 135 140

Pro Lys Asp Val Met Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Glu
 180 185 190

Leu Ala Thr Ala Tyr Ile Lys Pro Asp Glu Lys His His Ala Val Ile
 195 200 205

Ser Gly Ser Val Leu Tyr Asn Gln Asp Glu Lys Gly Ser Tyr Ser Leu
 210 215 220

Gly Ile Phe Gly Gly Gln Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240

Glu Thr Ala Asn Gly Ile His His Ile Gly Leu Ala Ala Lys Gln

216

245

250

255

<210> 235

<211> 768

<212> DNA

<213> *Neisseria meningitidis*

<400> 235

```

tgcagcagcg gagggcgcgg tgtcgccgcc gacatcggcg cggggcttgc cgatgcacta      60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcgcgc      120
aggaaaaacg agaaactgaa gctggcgggc caaggtgcgg aaaaaactta tggaaacggc      180
gacagcctta atacgggcaa attgaagaac gacaaggtca gccgtttcga ctttatccgt      240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca agtgtacaaa      300
caaagccatt ccgccttaac cgcccttcag accgagcaag aacaagatcc agagcattcc      360
gggaagatgg ttgcgaaacg ccggttcaaa atcggcgaca tagcgggcga acatacatct      420
tttgacaagc ttcccaaaga cgtcatggcg acatatcgcg ggacggcggt cggttcagac      480
gatgccggcg gaaaactgac ctatactata gattttgctg ccaaacaggg acacggcaaa      540
atcgaacatt tgaaatcgcc cgaactcaat gtcgagcttg ccaccgcta tatcaagccg      600
gatgaaaaac accatgccgt catcagcggg tccgtccttt acaatcaaga cgagaaaggc      660
agttactccc tcggtatctt tggcgggcaa gccaggaag ttgccggcag cgcggaagtg      720
gaaaccgcaa acggcataca ccatatcggt cttgccgccca agcaataa      768

```

<210> 236

<211> 255

<212> PRT

<213> *Neisseria meningitidis*

<400> 236

```

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10           15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
          20           25           30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35           40           45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50           55           60

```


217

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu
 100 105 110

Gln Glu Gln Asp Pro Glu His Ser Gly Lys Met Val Ala Lys Arg Arg
 115 120 125

Phe Lys Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
 130 135 140

Pro Lys Asp Val Met Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Glu
 180 185 190

Leu Ala Thr Ala Tyr Ile Lys Pro Asp Glu Lys His His Ala Val Ile
 195 200 205

Ser Gly Ser Val Leu Tyr Asn Gln Asp Glu Lys Gly Ser Tyr Ser Leu
 210 215 220

Gly Ile Phe Gly Gly Gln Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240

Glu Thr Ala Asn Gly Ile His His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 237

<211> 771

<212> DNA

<213> Neisseria meningitidis

<400> 237

tgccgatcca ggcgaggcgg cgggtgtcgcc gccgacatcg gcgcggggct tgccgatgca 60

218

```

ctaaccgcac cgctcgacca taaagacaaa agtttgacgt ctttgacgct ggatcagtcc 120
gtcaggaaaa acgagaaact gaagctggcg gcacaagggt cggaaaaaac ttatggaaac 180
ggcgacagcc ttaatacggg caaattgaag aacgacaagg tcagccggtt cgactttatc 240
cgtcaaactcg aagtggacgg gcagctcatt accttgagga gcggagagtt ccaagtgtac 300
aaacaaagcc attccgcctt aaccgcctt cagaccgagc aagaacaaga tccagagcat 360
tccgggaaga tggttgcgaa acgccggttc aaaatcggcg acatagcggg cgaacatata 420
tcttttgaca agcttcccaa agacgtcatg gcgacatatc gcgggacggc gttcggttca 480
gacgatgccg gcggaaaact gacctatact atagattttg ctgccaaaca gggacacggc 540
aaaatcgaac atttgaaatc gcccgaaactc aatgtcgagc ttgccaccgc ctatatcaag 600
ccggatgaaa aacaccatgc cgtcatcagc ggttcggtcc ttacaatca agacgagaaa 660
ggcagttact ccctcggtat ctttggcggg caagcccagg aagttgccgg cagcgcgga 720
gtggaaaccg caaacggcat acaccatatc ggtcttgccg ccaagcaata a 771

```

<210> 238

<211> 256

<212> PRT

<213> *Neisseria meningitidis*

<400> 238

```

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
1           5           10          15

```

```

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
20           25           30

```

```

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
35           40           45

```

```

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
50           55           60

```

```

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
65           70           75           80

```

```

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
85           90           95

```


219

Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr
 100 105 110

Glu Gln Glu Gln Asp Pro Glu His Ser Gly Lys Met Val Ala Lys Arg
 115 120 125

Arg Phe Lys Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys
 130 135 140

Leu Pro Lys Asp Val Met Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser
 145 150 155 160

Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys
 165 170 175

Gln Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val
 180 185 190

Glu Leu Ala Thr Ala Tyr Ile Lys Pro Asp Glu Lys His His Ala Val
 195 200 205

Ile Ser Gly Ser Val Leu Tyr Asn Gln Asp Glu Lys Gly Ser Tyr Ser
 210 215 220

Leu Gly Ile Phe Gly Gly Gln Ala Gln Glu Val Ala Gly Ser Ala Glu
 225 230 235 240

Val Glu Thr Ala Asn Gly Ile His His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 239

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 239

atgagcagcg gaggcggcgg tgtcgccgcc gacatcggcg cggggccttgc cgatgcacta	60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc	120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc	180
gacagcctta atacgggcaa attgaagaac gacaaggcca gccgtttcga ctttatccgt	240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca agtgtacaaa	300
caaagccatt ccgccttaac cgccttcag accgagcaag aacaagatcc agagcattcc	360

220

```

gggaagatgg ttgcgaaacg ccggttcaaa atcggcgaca tagcgggcga acatacatct      420
tttgacaagc ttcccaaaga cgtcatggcg acatatcgcg ggacggcggt cggttcagac      480
gatgccggcg gaaaactgac ctatactata gattttgctg ccaaacaggg acacggcaaa      540
atcgaacatt tgaaatcgcc cgaactcaat gtcgagcttg ccaccgccta tatcaagccg      600
gatgaaaaac accatgccgt catcagcggg tccgtccttt acaatcaaga cgagaaaggc      660
agttactccc tcggtatctt tggcgggcaa gccaggaag ttgccggcag cgcggaagtg      720
gaaaccgcaa acggcataca ccatatcggt cttgccgcca agcaataa                    768

```

```

<210> 240
<211> 255
<212> PRT
<213> Neisseria meningitidis

<400> 240

```

```

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1           5           10           15

```

```

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
          20           25           30

```

```

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
          35           40           45

```

```

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
          50           55           60

```

```

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65           70           75           80

```

```

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
          85           90           95

```

```

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu
          100          105          110

```

```

Gln Glu Gln Asp Pro Glu His Ser Gly Lys Met Val Ala Lys Arg Arg
          115          120          125

```

```

Phe Lys Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
          130          135          140

```


221

Pro Lys Asp Val Met Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Glu
 180 185 190

Leu Ala Thr Ala Tyr Ile Lys Pro Asp Glu Lys His His Ala Val Ile
 195 200 205

Ser Gly Ser Val Leu Tyr Asn Gln Asp Glu Lys Gly Ser Tyr Ser Leu
 210 215 220

Gly Ile Phe Gly Gly Gln Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240

Glu Thr Ala Asn Gly Ile His His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 241

<211> 765

<212> DNA

<213> *Neisseria meningitidis*

<400> 241

tgcagcagcg gaggcggcgg tgctcgccgcc gacatcggcg cggggccttgc cgatgcacta	60
accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc	120
aggaaaaacg agaaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc	180
gacagcctta atacgggcaa attgaagaac gacaagggtca gccgtttcga ctttatccgt	240
caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca agtgtacaaa	300
caaagccatt cgccttaac cgcccttcag accgagcaag aacaagatcc agagcattcc	360
gggaagatgg ttgcgaaacg ccggttcaaa atcggcgaca tagcgggga acatacatct	420
tttgacaagc ttcccaaaga cgatcatggcg acatatcgcg ggacggcggtt cggttcagac	480
gatgcgggcg gaaaactgac ctatactata gattttgctg ccaaacaggg acacggcaaa	540
atcgaacatt tgaaatcgcc cgaactcaat gtcgagcttg ccaccgccta tatcaagccg	600
gatgaaaaac accatgccgt catcagcggg tccgtccttt acaatcaaga cgagaaaggc	660

222

agttactccc tcggtatctt tggcgggcaa gcccaggaag ttgccggcag cgcggaagtg 720

gaaaccgcaa acggcatata ccatatcggt cttgccgcca agcaa 765

<210> 242

<211> 255

<212> PRT

<213> Neisseria meningitidis

<400> 242

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
85 90 95

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu
100 105 110

Gln Glu Gln Asp Pro Glu His Ser Gly Lys Met Val Ala Lys Arg Arg
115 120 125

Phe Lys Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
130 135 140

Pro Lys Asp Val Met Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
165 170 175

223

Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Glu
 180 185 190

Leu Ala Thr Ala Tyr Ile Lys Pro Asp Glu Lys His His Ala Val Ile
 195 200 205

Ser Gly Ser Val Leu Tyr Asn Gln Asp Glu Lys Gly Ser Tyr Ser Leu
 210 215 220

Gly Ile Phe Gly Gly Gln Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240

Glu Thr Ala Asn Gly Ile His His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 243

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 243

tgcggtacca gcgaggcg cggtgtcgcc gccgacatcg gcgcggggct tgccgatgca	60
ctaaccgcac cgctcgacca taaagacaaa agtttgagct ctttgacgct ggatcagtc	120
gtcaggaaaa acgagaaaact gaagctggcg gcacaaggtg cggaaaaaac ttatggaaac	180
ggcgacagcc ttaatacggg caaattgaag aacgacaagg tcagccgttt cgactttatc	240
cgtcaaatacg aagtggacgg gcagctcatt accttgagga gcggagagtt ccaagtgtac	300
aaacaaagcc attccgcctt aaccgcccctt cagaccgagc aagaacaaga tccagagcat	360
tccgggaaga tggttgcgaa acgccggttc aaaatcgggc acatagcggg cgaacataca	420
tcttttgaca agcttcccaa agacgtcatg gcgacatatc gcgggacggc gttcggttca	480
gacgatgccg gcggaaaact gacctatact atagattttg ctgccaaaaca gggacacggc	540
aaaatcgaac atttgaaatc gcccgaactc aatgtcgagc ttgccaccgc ctatatcaag	600
ccggatgaaa aacaccatgc cgatcatcagc gggtccgtcc tttacaatca agacgagaaa	660
ggcagttact ccctcggtat ctttggcggg caagcccagg aagttgccgg cagcgcggaa	720
gtggaaaccg caaacggcat acaccatatc ggtcttgccg ccaagcaa	768

<210> 244

<211> 256

<212> PRT

<213> Neisseria meningitidis

224

<400> 244

Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly
 1 5 10 15

Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu
 20 25 30

Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys
 35 40 45

Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu
 50 55 60

Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile
 65 70 75 80

Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu
 85 90 95

Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr
 100 105 110

Glu Gln Glu Gln Asp Pro Glu His Ser Gly Lys Met Val Ala Lys Arg
 115 120 125

Arg Phe Lys Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys
 130 135 140

Leu Pro Lys Asp Val Met Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser
 145 150 155 160

Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys
 165 170 175

Gln Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val
 180 185 190

Glu Leu Ala Thr Ala Tyr Ile Lys Pro Asp Glu Lys His His Ala Val
 195 200 205

Ile Ser Gly Ser Val Leu Tyr Asn Gln Asp Glu Lys Gly Ser Tyr Ser
 210 215 220

225

Leu Gly Ile Phe Gly Gly Gln Ala Gln Glu Val Ala Gly Ser Ala Glu
 225 230 235 240

Val Glu Thr Ala Asn Gly Ile His His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 245

<211> 765

<212> DNA

<213> Neisseria meningitidis

<400> 245

atgagcagcg gagggcgcgg tgtcgccgcc gacatcgggc cggggccttgc cgatgcacta 60
 accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc 120
 aggaaaaacg agaaactgaa gctggcgggc caaggtgcgg aaaaaactta tggaaacggc 180
 gacagcctta atacgggcaa attgaagaac gacaaggtca gccgtttcga ctttatccgt 240
 caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca agtgtacaaa 300
 caaagccatt ccgccttaac cgcccttcag accgagcaag aacaagatcc agagcattcc 360
 gggaagatgg ttgcgaaacg ccggttcaaa atcggcgaca tagcggggcg acatacatct 420
 ttgacaagc ttcccaaaga cgtcatggcg acatatcgcg ggacggcggt cggttcagac 480
 gatgccggcg gaaaactgac ctatactata gatatttgctg ccaaacaggg acacggcaaa 540
 atcgaacatt tgaaatcgcc cgaactcaat gtcgagcttg ccaccgccta tatcaagccg 600
 gatgaaaaac accatgccgt catcagcggg tccgtccttt acaatcaaga cgagaaaggc 660
 agttactccc tcggtatctt tggcggggcaa gccaggaag ttgccggcag cgcggaagtg 720
 gaaaccgcaa acggcataca ccatatcggt cttgccgccca agcaa 765

<210> 246

<211> 255

<212> PRT

<213> Neisseria meningitidis

<400> 246

Met Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

226

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu
 100 105 110

Gln Glu Gln Asp Pro Glu His Ser Gly Lys Met Val Ala Lys Arg Arg
 115 120 125

Phe Lys Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
 130 135 140

Pro Lys Asp Val Met Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Glu
 180 185 190

Leu Ala Thr Ala Tyr Ile Lys Pro Asp Glu Lys His His Ala Val Ile
 195 200 205

Ser Gly Ser Val Leu Tyr Asn Gln Asp Glu Lys Gly Ser Tyr Ser Leu
 210 215 220

Gly Ile Phe Gly Gly Gln Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240

Glu Thr Ala Asn Gly Ile His His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

227

<210> 247
 <211> 783
 <212> DNA
 <213> *Neisseria meningitidis*

<400> 247
 tgcagcagcg gaggcggcgg aagcggaggc ggcggtgtca ccgccgacat cggcacgggg 60
 cttgccgatg cactaactgc gccgctcgac cataaagaca aaggcttgaa atccctgaca 120
 ttggaagact ccatttccca aaacggaaca ctgaccctgt cggcacaagg tgcggaaaaa 180
 acttatggaa acggcgacag ccttaatacg ggcaaattga agaacgacaa ggtcagccgt 240
 ttcgacttta tccgtcaaat cgaagtggac gggcagctca ttaccttgga gagcggagag 300
 ttccaagtgt acaaacaag ccattccgcc ttaaccgccc ttcagaccga gcaagaacaa 360
 gatccagagc attccgagaa gatggttgcg aaacgccggg tcagaatcgg cgacatagcg 420
 ggcgaacata catcttttga caagcttccc aaagacgtca tggcgacata tcgcgggacg 480
 gcgttcgggt cagacgatgc cggcggaaaa ctgacctata ctatagattt tgctgccaaa 540
 cagggacacg gcaaaatcga acatttgaaa tcgccggaac tcaatgtcga tctggccgtc 600
 gcctatatca agccggatga aaaacaccat gccgtcatca gcggttcctg tctttacaac 660
 caagacgaga aaggcagtta ctccctcggg atctttggcg aaaaagccca ggaagttgcc 720
 ggcagcgcgg aagtggaaac cgcaaacggc atacaccata tcggtcttgc cgccaagcag 780
 taa 783

<210> 248
 <211> 260
 <212> PRT
 <213> *Neisseria meningitidis*

<400> 248

Cys Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Val Thr Ala Asp
 1 5 10 15

Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys
 20 25 30

Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn
 35 40 45

Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn
 50 55 60

228

Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg
 65 70 75 80

Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu
 85 90 95

Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr
 100 105 110

Ala Leu Gln Thr Glu Gln Glu Gln Asp Pro Glu His Ser Glu Lys Met
 115 120 125

Val Ala Lys Arg Arg Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr
 130 135 140

Ser Phe Asp Lys Leu Pro Lys Asp Val Met Ala Thr Tyr Arg Gly Thr
 145 150 155 160

Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp
 165 170 175

Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Ser Pro
 180 185 190

Glu Leu Asn Val Asp Leu Ala Val Ala Tyr Ile Lys Pro Asp Glu Lys
 195 200 205

His His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn Gln Asp Glu Lys
 210 215 220

Gly Ser Tyr Ser Leu Gly Ile Phe Gly Glu Lys Ala Gln Glu Val Ala
 225 230 235 240

Gly Ser Ala Glu Val Glu Thr Ala Asn Gly Ile His His Ile Gly Leu
 245 250 255

Ala Ala Lys Gln
 260

<210> 249

<211> 786

<212> DNA

<213> Neisseria meningitidis

229

<400> 249
 tgcggatcca gcggaggcgg cggaagcgga ggcggcggtg tcaccgccga catcggcacg 60
 gggcttgccg atgcactaac tgcgcgcgtc gaccataaag acaaaggctt gaaatccctg 120
 acattggaag actccatttc ccaaaacgga acactgaccc tgtcggcaca aggtgcggaa 180
 aaaacttatg gaaacggcga cagccttaat acggggcaaat tgaagaacga caaggtcagc 240
 cgtttcgact ttatccgtca aatcgaagtg gacgggcagc tcattacctt ggagagcgga 300
 gagttccaag tgtacaaaca aagccattcc gccttaaccg cccttcagac cgagcaagaa 360
 caagatccag agcattccga gaagatggtt gcgaaacgcc gggttcagaat cggcgacata 420
 gcgggcgaac atacatcttt tgacaagctt ccaaagacg tcatggcgac atatcgcggg 480
 acggcgttcg gttcagacga tgccggcgga aaactgacct atactataga ttttgctgcc 540
 aaacagggac acggcaaaat cgaacatttg aaatcgccgg aactcaatgt cgatctggcc 600
 gtcgcctata tcaagccgga tgaaaaacac catgccgtca tcagcggttc cgttctttac 660
 aaccaagacg agaaaggcag ttactccctc ggtatctttg gcgaaaaagc ccaggaagtt 720
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 35 40 45
 Asn Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Tyr Gly
 50 55 60
 Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser
 65 70 75 80

230

Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr
 85 90 95

Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu
 100 105 110

Thr Ala Leu Gln Thr Glu Gln Glu Gln Asp Pro Glu His Ser Glu Lys
 115 120 125

Met Val Ala Lys Arg Arg Phe Arg Ile Gly Asp Ile Ala Gly Glu His
 130 135 140

Thr Ser Phe Asp Lys Leu Pro Lys Asp Val Met Ala Thr Tyr Arg Gly
 145 150 155 160

Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile
 165 170 175

Asp Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Ser
 180 185 190

Pro Glu Leu Asn Val Asp Leu Ala Val Ala Tyr Ile Lys Pro Asp Glu
 195 200 205

Lys His His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn Gln Asp Glu
 210 215 220

Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Glu Lys Ala Gln Glu Val
 225 230 235 240

Ala Gly Ser Ala Glu Val Glu Thr Ala Asn Gly Ile His His Ile Gly
 245 250 255

Leu Ala Ala Lys Gln
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<212> DNA

<213> Neisseria meningitidis

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acttatggaa acggcgacag ccttaatacg ggcaaattga agaacgacaa ggtcagccgt    240
ttcgacttta tccgtcaa at cgaagtggac gggcagctca ttaccttgga gagcggagag    300
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gatccagagc attccgagaa gatgggttgcg aaacgccggt tcagaatcgg cgacatagcg    420
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gcgttcgggt cagacgatgc cggcggaaaa ctgacctata ctatagattt tgctgccaaa    540
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gcctatatca agccggatga aaaacaccat gccgtcatca gcggttcctg tctttacaac    660
caagacgaga aaggcagtta ctccctcggg atctttggcg aaaaagccca ggaagttgcc    720
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<213> *Neisseria meningitidis*

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35           40           45

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Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn
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Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg
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Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu
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232

Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr
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Ala Leu Gln Thr Glu Gln Glu Gln Asp Pro Glu His Ser Glu Lys Met
 115 120 125

Val Ala Lys Arg Arg Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr
 130 135 140

Ser Phe Asp Lys Leu Pro Lys Asp Val Met Ala Thr Tyr Arg Gly Thr
 145 150 155 160

Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp
 165 170 175

Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Ser Pro
 180 185 190

Glu Leu Asn Val Asp Leu Ala Val Ala Tyr Ile Lys Pro Asp Glu Lys
 195 200 205

His His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn Gln Asp Glu Lys
 210 215 220

Gly Ser Tyr Ser Leu Gly Ile Phe Gly Glu Lys Ala Gln Glu Val Ala
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Ala Ala Lys Gln
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gctggcggaa aactgacctt taccatagat ttgcgcgcca aacagggaca cggcaaaatc 180

233

gaacacctga aaacacccga gcaaaatgtc gagcttgccg ccgccgaact caaagcagat 240
gaaaaatcac acgccgtcat ttggggcgac acgcgctacg gcagcgaaga aaaaggcact 300
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<213> *Neisseria meningitidis*

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Ser Gly Glu Phe Gln Ile Tyr Lys Gln
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His Ser Ala Val Val Ala Leu Gln Ile Glu
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Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp
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Gly Glu His Thr Ala Phe Asn Gln Leu Pro
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Leu Pro

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Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
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Lys Thr Pro Glu Gln Asn Val Glu Leu Ala
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Glu His Thr Ser Phe Asp Lys Leu Pro Lys
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Ser Leu Thr Leu Xaa Xaa Ser Xaa Xaa Xaa Asn Xaa Xaa Leu Xaa Leu
 35 40 45

Xaa Ala Gln Gly Ala Glu Lys Thr Xaa Xaa Xaa Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Xaa Ser Arg Phe Asp Phe Xaa Xaa
 65 70 75 80

Xaa Ile Xaa Val Asp Gly Xaa Xaa Ile Thr Leu Xaa Ser Gly Glu Phe
 85 90 95

Gln Xaa Tyr Lys Gln Xaa His Ser Ala Xaa Xaa Ala Leu Gln Xaa Glu
 100 105 110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa
 115 120 125

Phe Xaa Xaa Xaa Xaa Xaa Xaa Gly Glu His Thr Xaa Phe Xaa Xaa Leu
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Pro Xaa Xaa Xaa Ala Xaa Tyr Xaa Gly Xaa Ala Phe Xaa Ser Asp Asp
 145 150 155 160

Xaa Xaa Gly Xaa Leu Xaa Tyr Xaa Ile Asp Phe Xaa Xaa Lys Gln Gly
 165 170 175

Xaa Gly Xaa Ile Glu His Leu Lys Xaa Pro Glu Xaa Asn Val Xaa Leu
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Ala Xaa Xaa Xaa Xaa Lys Xaa Asp Glu Lys Xaa His Ala Val Ile Xaa
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Gly Xaa Xaa Xaa Tyr Xaa Xaa Xaa Glu Lys Gly Xaa Tyr Xaa Leu Xaa
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Xaa Xaa Gly Xaa Xaa Ala Gln Glu Xaa Ala Gly Xaa Ala Xaa Val Xaa
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35 40 45

Xaa Ala Gln Gly Ala Glu Lys Thr Xaa Xaa Xaa Gly Asp Ser Leu Asn
50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Xaa Ser Arg Phe Asp Phe Xaa Xaa
65 70 75 80

Xaa Ile Xaa Val Asp Gly Gln Xaa Ile Thr Leu Xaa Ser Gly Glu Phe

261

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Gln Ile Tyr Lys Gln Xaa His Ser Ala Val Val Ala Leu Gln Ile Glu	100		105		110	
Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser	115		120		125	
Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu	130		135		140	
Pro Xaa Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp	145		150		155	160
Xaa Xaa Gly Xaa Leu Xaa Tyr Xaa Ile Asp Phe Xaa Xaa Lys Gln Gly	165		170		175	
Xaa Gly Xaa Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu	180		185		190	
Ala Xaa Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu	195		200		205	
Gly Asp Thr Arg Tyr Gly Xaa Glu Glu Lys Gly Thr Tyr His Leu Ala	210		215		220	
Leu Xaa Gly Asp Arg Ala Gln Glu Ile Ala Gly Xaa Ala Thr Val Lys	225		230		235	240
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Ser Leu Thr Leu Xaa Xaa Ser Xaa Xaa Xaa Asn Xaa Xaa Leu Xaa Leu
 35 40 45

Xaa Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80

Gln Ile Glu Val Asp Gly Xaa Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95

Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu
 100 105 110

Gln Xaa Gln Asp Xaa Glu Xaa Ser Xaa Lys Met Val Ala Lys Arg Xaa
 115 120 125

Phe Xaa Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
 130 135 140

Pro Lys Xaa Xaa Xaa Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175

Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Xaa
 180 185 190

Leu Ala Xaa Xaa Tyr Ile Lys Pro Asp Glu Lys Xaa His Ala Val Ile
 195 200 205

Ser Gly Ser Val Leu Tyr Asn Gln Asp Glu Lys Gly Ser Tyr Ser Leu
 210 215 220

Gly Ile Phe Gly Xaa Xaa Ala Gln Glu Val Ala Gly Ser Ala Glu Val
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266

245

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Cys Ser Pro Ala Ala Asp Ser Asn His Pro Ser Gly Gln Asn Ala Pro
 1 5 10 15

Ala Asn Thr Glu Ser Asp Gly Lys Asn Ile Thr Leu Leu Asn Ala Ser
 20 25 30

Tyr Asp Val Ala Arg Asp Phe Tyr Lys Glu Tyr Asn Pro Leu Phe Ile
 35 40 45

Lys Thr Tyr Gln Ser Glu His Pro Gly Thr Ser Val Ser Ile Gln Gln
 50 55 60

Ser His Gly Gly Ser Ser Lys Gln Ala Leu Ser Val Ala Asn Gly Leu
 65 70 75 80

272

Gln Ala Asp Val Val Thr Met Asn Gln Ser Ser Asp Ile Asp Leu Leu
85 90 95

Glu Lys Lys Gly Leu Val Glu Lys Gly Trp Gln Gln Ala Leu Pro Asp
100 105 110

His Ala Ala Pro Tyr Thr Ser Thr Met Val Phe Leu Val Arg Lys Asn
115 120 125

Asn Pro Lys Gln Ile Arg Asp Trp Asn Asp Leu Ala Lys Asp Gly Val
130 135 140

Asn Ile Val Ile Ala Asn Pro Lys Thr Ser Gly Asn Gly Arg Tyr Ala
145 150 155 160

Phe Leu Gly Ala Tyr Gly Tyr Gly Leu Lys Thr Thr Asn Gly Asn Glu
165 170 175

Gln Glu Ala Gln Lys Leu Val Ala Ser Ile Leu Lys Asn Thr Pro Val
180 185 190

Phe Glu Asn Gly Gly Arg Ala Ala Thr Thr Thr Phe Thr Gln Arg Asn
195 200 205

Ile Gly Asp Val Leu Ile Thr Phe Glu Asn Glu Ala Asn Tyr Val Ser
210 215 220

Lys Lys Leu Thr Gln Gly Gln Phe Glu Ile Val Tyr Pro Ser Tyr Thr
225 230 235 240

Ile Ser Ala Glu Ser Pro Val Ala Val Val Asn Ser Val Val Ala Lys
245 250 255

Lys Gly Thr Gln Lys Thr Ala Arg Ala Tyr Leu Glu Tyr Leu Trp Ser
260 265 270

Glu Pro Ala Gln Glu Leu Ala Ala Ser Leu Tyr Leu Arg Pro Arg Asn
275 280 285

Pro Glu Val Leu Ala Arg His Lys Ala Asp Phe Pro Asp Leu Asp Thr
290 295 300

Phe Ser Pro Glu Glu Lys Phe Gly Gly Trp Asp Asn Ile Met Lys Thr

273

305

310

315

320

Tyr Phe Ala Asp Gly Gly Ile Phe Asp Arg Leu Thr Ala Gln Lys
 325 330 335

<210> 328

<211> 68

<212> PRT

<213> Neisseria meningitidis

<400> 328

Cys Ala Gly Thr Trp Glu Gly Ala Lys Gln Asp Thr Ala Arg Asn Leu
 1 5 10 15

Asp Lys Thr Gln Ala Ala Ala Glu Arg Ala Ala Glu Gln Thr Gly Asn
 20 25 30

Ala Val Glu Lys Gly Trp Asp Lys Thr Lys Glu Ala Val Lys Lys Gly
 35 40 45

Gly Asn Ala Val Gly Arg Gly Ile Ser His Leu Gly Gly Lys Ile Glu
 50 55 60

Asn Ala Thr Glu
 65

<210> 329

<211> 21

<212> PRT

<213> Neisseria meningitidis

<400> 329

Cys Met Lys Thr Thr Leu Lys Met Thr Ala Leu Ala Ala Leu Ser Ala
 1 5 10 15

Phe Val Leu Ala Gly
 20